

### STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 151497

TO: Sumesh Kaushal

Location: REM-2B85/2C70

Art Unit: 1636

Wednesday, April 27, 2005

Case Serial Number: 10/735014

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen 1a69

Phone: 571-272-2518

barbara.obryen@uspto.gov

#### Search Notes



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Ada38026
Ada21712 F
Ada18043 F
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Ada38151 F
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Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
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ABU10960
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ABU67135
ABU81712
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ADA10499
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Searched:

Chen J;

Result Š. 2000WO-US005841

02-MAR-2000;

14-SEP-2000

WO200053758-A2 Homo sapiens.

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The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have activated, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polymuclectides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agoniets and antagoniets are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic colerosis, idiopathic inflammatory myopathies, Sjogren's systemic eclerosis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
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Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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99US-0145698P.
99US-0146222P.
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Kabakoff RC,
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Hillan KJ, Kljavin IJ,
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peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleocide and protein sequences given in the exemplification of the present invention
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                                                                                                                                 Query Match 100.0%; Score 2211; DB 3; Best Local Similarity 100.0%; Pred. No. 4.9e-173; Matches 431; Conservative 0; Mismatches 0;
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/label= Signal peptide
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/note=
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                                                                                                              Sequence 431 AA;
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16, Goddard A, Godowski PJ, Grimaldi CJ, Gurney
Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood W
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"Tyrosine kinase phosphorylation site"
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100.0%; Pred. No. 4.9e-173;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "cAMP- and cGMP-dependent
                                                                                                                                                                                                                                                                                                                                                     /note= "N-glycosylation site"
384. .405
/label= Transmembrane domain
                                                       "N-glycosylation site"
                                                                                   "N-glycosylation site"
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                                                                                                                                                                                                                                                                                                   /note= "N-glycosylation
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/note= "CAMP- and cGM
phosphorylation site"
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                                                                                      EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLGRILSESLRRKRYSRL 420
                                                                                                                           EASPGSSSOGSVPENOYGLPFEKWLLIGSLLFGVLFLVIGLVLIGRILSESLRRKRYSRL 420
                                                                                                                                                                                                                                                                                                                           systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke; hematootasis regulation; tissue regrowth; wound healing; haemophilia; Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer; contraceptive; infection; growth inhibition; hyperproliferative disorder;
                                                   TPKFATLLPTNASVTPSGTSOPOLATTAPPVTTVTSOPPTTLISTVFTRAAATLOAMATT 300
                                                                                                                                                                                                                                                                                                             Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
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AVLTTTPQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
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sclerosis, systemic lupus erythmatosus, rheumatoid arthritis, cancer,
Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.
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                                                                                                                                                                                                                                                                                            Human secreted protein encoded by DNA clone vo27 1.
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99US-0149639P.
99US-0157247P.
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17-AUG-1999;
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ancipacterial, virtuines, and rungitime activity: The proteins are useful as nutritional sources or supplements and in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, autoimmune deficiency and disorders, which may be genetic or resulting from infections, autoimmune deficiencies such as anaemias by regulating hematopolesis. The proteins of deficiencies such as anaemias by regulating hematopolesis. The proteins are also useful in compositions for bone, cartilage, tendon, ligament and roplacement and in the treatment of wounds, incisions and culcers. Other uses include in the treatment of wounds, incisions and culcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's culcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's such as spinal cord disorders, head trauma and stroke. The proteins may also be used as a contraceptive, and for treating coagulation disorders, such as heamophilas. The protein and nucleotide sequences with cadherin activity are useful for treating commer. Other uses for the protein culcude for inhibiting the growth, infection or function of, or killing, infecting bodily characteristics such as height, weight, hair colour, effecting biorhythms or cardiac cycles or rhythms, effecting metabolism, anabolism, processing, utilization, storage or elimination of cateabolism, anabolism, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics providing analgesic effects and ceffecting behavioural characteristics such as psoriasis
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; Pred. No. 4.9e-173;
0; Mismatches 0; Indels 0
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Best Local Similarity 100.
Matches 431; Conservative
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300
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Godowski PJ;
Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted and transmembrane protein; PRO; cytostatic, cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                HLBKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                                                                                                                                                       241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
                                                                                                                                                                                                                                        EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
      HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQE1AHLLPENVSALPATVAVASPHTTSA
                                                                                 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
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Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO361 protein sequence SEQ ID NO:515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB65299 standard; protein; 431 AA.
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99US-0145698P.
99US-0146222P.
99US-0149396P.
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99WO-US028301,
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01-DEC-1999
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20-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification, Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the complementary strand of a polynucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the comprises at least 15 nucleotides and the combination of the 5'-end sequence[3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers sets can be used in antisense therapy and in geneticiarly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13613 to AAH13623 represent human amino acid sequences; and AAH13629 to AAH13612 represent considered in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                      primer; detection; diagnosis; antisense therapy; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID NO 17950; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                               ogai T, Nishikawa T, Hayashi K, Saito K, Y.
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
Human protein sequence SEQ ID NO:17950.
                                                                                                                                                                                                                                  99JP-00248036.
99JP-00300253.
2000JP-00118776.
2000JP-00183767.
                                                                                                                                                                                               28-JUL-2000; 2000EP-00116126
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Matches 431; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 431 AA;
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02-MAY-2000;
09-JUN-2000;
                                                                                                                    EP1074617-A2.
                                                                               Homo sapiens
                                                                                                                                                                                                                                      29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                      Human;
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Human, PRO; secreted protein, transmembrane protein, anti-HIV; cytostatic, antiatriatiosderotic; antiinflammatory, antidiabetic; cardiant, AIDS; acquired immunodeficiency syndrome; cancer, atherosclerosis; inflammatory disease; diabetic complication;

cardiac injury; organ failure

31-AUG-2001; 2001US-00944654

US2002142959-A1

03-OCT-2002

Homo sapiens.

Human secreted/transmembrane protein PRO361.

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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4420 to AAF44470 represent PCR primers and hybridisation probes used in the labolation of human PRO sequences. AAF44687 to AAF4453 and AAB65154 to AAF85500 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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                                                                                                                                                                                             PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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Watanabe CK, Williams PM, Wood WI;
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100.0%; Pred. No. 4.9e-173;
ive 0; Mismatches 0;
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Tumas D,
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Best Local Similarity 100.
Matches 431; Conservative
   Stewart TA,
                                                                                           WPI; 2001-032160/04
                                                                                                                                N-PSDB; AAF44268
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   Ă,
   Roy MA
Zhang
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The invention relates to an isolated PRO polypeptide (a secreted or transmembrane protein) comprising: (a) at least 80% sequence identity or constitutes when compared to any of 15 sequences; fully defined in the specification, lacking or with its associated signal peptide; or (b) at specification, lacking or with its associated signal peptide; or (b) at least 80% sequence encoded by the full-length coding sequence of a DNA deposited in the American Type Culture CC coling sequence of a DNA deposited in the American Type Culture as a RNO protein; (b) at least 80% sequence identity to a nucleotide sequence contains a proportion; (b) at least 80% sequence identity to a nucleotide sequence or full-length coding sequence identity to a nucleotide sequence or full-length coding sequence identity to a nucleotide sequence or full-length coding sequence of a construction of the specification; or (c) at least 80% sequence identity to a nucleotide sequence of a coding sequence identity to a nucleotide sequence of a coding sequence identity to a coding sequence of a coding sequence identity to a nucleotide sequence of a coding sequence identity to a coding sequence of a coding sequence identity to a coding sequence of a coding sequence identity as vector comprising the vector comprising the vector comprising the vector which, when cultured under conditions suitable coding sequence; and (5) a nati-post of the present invention are useful for the diagnosis and treatment of the present invention are useful for the diagnosis and treatment of immunodeficiency syndrome), cancer, atherosclerosis, inflammatory disease, diabetic complications, cardiac injury and organ failure. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
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Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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2000WO-US008439.
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2000WO-US032678.
2001WO-US006520.
99WO-US012252
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99WO-US028409
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Hillan KJ, Kljavin IJ, N
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N-PSDB; ABX75504.
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01-DEC-2000;
28-FEB-2001;
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22-JUN-1999
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EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL

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DYLINGIYVDI 431 DYLINGIYVDI

ABU55934 standard; protein; 431 AA

RESULT 7 ABU55934

(first entry)

26-MAR-2003 ABU55934;

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9805-0087106P-
9808-0087106P-
9808-0087107P-
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9808-0099028P-
9808-0099024P-
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98US-0091544P.
98US-0091478P.
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antibodies can also be used in the different screening, therapeutic and biological assays. The present sequence represents a PRO protein
                                                                                                                                              1 MPFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIOSSLSKGIRGNEPVYTSTO
                                                                                                                                                                                                                                                                HLEKL FKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
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                                                                                                      Gaps
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horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
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0
                                                                        Length 431;
                                                                                                    0; Indels
                                                                  Query Match 100.0%; Score 2211; DB 6; Best Local Similarity 100.0%; Pred. No. 4.9e-173; Matches 431; Conservative 0; Mismatches 0;
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97UG-0062250P.
97UG-0065318P.
97US-0065311P.
97US-0066770P.
98US-0075945P.
98US-0075945P.
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17-OCT-1997;
05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
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20-MAR-1998;
28-APR-1998;
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26-AUG-1998;
31-AUG-1998;
11-SEP-1998;
16-SEP-1998;
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17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
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02-JUN-1999
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0; Indels
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ABU59192
ID ABU59192 standard; protein; 431 AA
XX
AC ABU59192;
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DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembr
XX
16-DEC-1999; 99WO-US030095.
C5-JAN-2000; 2000WO-US030911.
C6-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US00376.
12-FEB-2000; 2000WO-US00341.
22-FEB-2000; 2000WO-US004414.
24-FEB-2000; 2000WO-US004114.
24-FEB-2000; 2000WO-US004114.
24-FEB-2000; 2000WO-US004114.
24-FEB-2000; 2000WO-US006114.
24-FEB-2000; 2000WO-US006114.
24-FEB-2000; 2000WO-US006114.
24-FEB-2000; 2000WO-US016119.
15-WAR-2000; 2000WO-US01377.
20-WAY-2000; 2000WO-US01376.
17-WAY-2000; 2000WO-US01376.
17-WAY-2000; 2000WO-US01376.
23-WAY-2000; 2000WO-US01376.
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23-WAY-2000; 2000WO-US01361.
23-WAY-2000; 2000WO-US01361.
24-AUG-2000; 2000WO-US023318.
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neonatal heart; angiogenesis; wound healing;
Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; endothelial growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
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                                                                         Homo sapiens.
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Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams
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                      99WO-US021547.
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Perrara N. Fong S, Gerber
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Godowski PJ; Paoni NF; Wood WI;

WPI; 2003-247083/24. N-PSDB; ABX80473.

PR01346 Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments

Claim 12; Fig 328; 648pp; English.

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in inking a bioactive molecule to a cell expressing a RO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus cusful for treating cardiac insufficiency disorders. PRO156, PRO186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO826, PRO186 or PRO535, PRO816, PRO943, PRO826, PRO186 or PRO535, PRO816, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth. PRO826, mammals which would be beneficial in inhibiting tumour growth.

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         stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813 and PRO11066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1130, PRO814, PRO1132, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
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 PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
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iive 0; Mismatches 0;
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100.0%;
Best Local Similarity 100.0%;
Matches 431; Conservative 0 99US-0123957P 99WO-US012252 08-MAR-1999; 12-MAR-1999; 07-JUN-1999; 07-JUN-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 15-SEP-1999; 15-SEP-1999; 15-SEP-1999; 16-DEC-1999; 01-DEC-1999; 01-DEC-1999; 01-DEC-1999; 06-JAN-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 24-FEB-2000; 26-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-MAY-2000; ч -4 61 61 g 8 S S ò

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Zhang Z;
Human, PRO; secreted; transmembrane; signal peptide; pharmaceutical;
diagnostic; therapeutic; gene therapy.
                                                 Human secreted/transmembrane protein, #182.
                    ABU60623 standard; protein; 431 AA.
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99WO-US012252
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28-FEB-2001;
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## (GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; Poy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

### WPI; 2003-288106/28. N-PSDB; ABX90451.

New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.

# Claim 12; Fig 328; 650pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or proteins at least polypuclectides are also useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO olypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

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98US-0078910P

98US-008332P

98US-0087607P

98US-0087609P

98US-0087759P

98US-0087759P

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98US-0088028P

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28 - MAX - 1998;
20 - JUN - 1998;
02 - JUN - 1998;
03 - JUN - 1998;
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PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ABU60478-ABU60624 are the PRO polynucleotides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html
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                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, PRO polypeptide, secreted protein; transmembrane protein; genetic disorder; antibacterial; immunosuppressive.
                                                                                               ;
                                                                          Query Match
100.0%; Score 2211; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.9e-173;
Matches 431; Conservative 0; Mismatches 0; Indels 0
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97US-0062250P.
97WS-0063186P.
97US-0065311P.
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05-NOV-1997;
12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
25-FEB-1998;
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Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer; inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility; birth defect; premature aging; diabetes; dog; cat; horse; acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit;
241 TPKRATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT
                                                           AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTWNKTASWEGR
                                                                                  301 AVLTTTFQAPIDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR
                                                                                                                                            EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSBSLRRKRYSRL
                                                                                                                                                                   EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acquired immunodeficiency syndrome; cow; sheep; pig; goat; rabbit; industry; cytostatic; antiinflammatory; cardiant; antiinfertility;
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97US-0069238P.
97US-00693354P.
97US-006964P.
97US-0069694P.
97US-0069702P.
97US-0069702P.
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polypeptides, and the polynucleotide sequences encoding them. The PRO
colypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for linking
polypeptides are useful for detecting other PRO polypeptides, for modulating
colipogical activities of cells expressing PRO polypeptides, for modulating
colipogical activities or antagonists. The pRO polypeptides, and for for
identifying agonists or antagonists. The polynucleotide sequences
concoding PRO polypeptides are useful as hybridisation probes, in
chromosome and gene mapping, in the generating probes, in
chromosome and gene mapping, in the generating transgenic animals,
in the preparation of PRO polypeptides, for generating probes, in
cor knockout animals, to construct hybridisation probes for mapping the
gene which encodes the PRO polypeptides, in gene therapy, for chromosome
condition, as chromosome markers, and for the genetic analysis of
induitication, as chromosome markers, and for generating probes for PCR,
Northern analysis, Southern analysis and Western analysis, ABU13860-
ABU14006 represent the human PRO polypeptides of the invention. Note: The
from the preparation of properties and for generating processing the form the properties of the invention of the properties.
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                                                                                                                                                                                                                                                                                                                                                         PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                                  DL;
Godowski P
Paoni NF;
Wood WI;
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                                                                                                                                                                                                                                                                                                                                    Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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23-AUG-2000; 2000WO-US02322.
24-AUG-2000; 2000WO-US033328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FBB-2001; 2011WO-US056520.
                                                                                                                                                                   01-JUN-2001; 2001WO-US017800.
20-JUN-2001; 2001WO-US019692.
29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
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Best Local Similarity
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US2003003531-A1
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04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
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                                                                           ABU72590;
                   RESULT 14
ABU72590
                                                             ö
                                                                                                                                                                                                                                                                                                                         The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, disquoretics, biosensors or bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
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                                                                                                                                                                                                                            New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
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Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL,
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                  Claim 1; Fig 32; 173pp; English.
30-MAR-2000; 2000MO-US008439.
22-MAY-2000; 2000MO-US014042.
28-JUL-2000; 2000MO-US020710.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US0066520.
25-MAY-2001; 2001US-00866028.
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Matches 431; Conservative
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N-PSDB; ABX89495.
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30-NOV-1999; 99W0-US021547.
30-NOV-1999; 99W0-US021547.
30-NOV-1999; 99W0-US028634.
30-DEC-1999; 99W0-US028634.
30-DEC-1999; 99W0-US028634.
30-DEC-1999; 99W0-US028634.
31-FEB-2000; 2000W0-US000316.
31-FEB-2000; 2000W0-US004341.
32-FEB-2000; 2000W0-US004341.
32-FEB-2000; 2000W0-US004341.
32-FEB-2000; 2000W0-US004341.
32-FEB-2000; 2000W0-US004341.
32-FEB-2000; 2000W0-US004341.
34-FEB-2000; 2000W0-US006841.
35-MAR-2000; 2000W0-US006841.
36-MAR-2000; 2000W0-US00684.
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23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US0303578.
01-DEC-2000; 2000WO-US030578.
28-FEB-2001; 2001WO-US030578.
01-JUN-2001; 2001WO-US017800.
98US-0089801P.
98US-0089907P.
98US-0089908P.
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2000WO-US014941.
2000WO-US015264.
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98WO-US019437.
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99WO-US012252
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                                              98WO-US021141
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17-MAY-2000; 2
22-MAY-2000; 2
30-MAY-2000; 2
02-JUN-2000; 2
28-JUL-2000; 2
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18-JUN-1998;
18-JUN-1998;
16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
01-DEC-1999;
05-JAN-1999;
05-JAN-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATC Deposit No. 20961, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Claim 12; Fig 328; 663pp; English.

ö EASPGSSSQGSVPENQYGLPFEKMLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420 240 240 360 120 120 180 180 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300 300 360 leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide 9 9 1 MFFGGEGSLIYTLVIICFLTLKLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD TPKPATILIPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 1 MFFGGEGSLTYTLVIICFLTLEASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEBACPLKPAKGLMSYRII 121 TDFPSLTRNLPSQELPQEDSLIHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR Gaps 0; Length 431; Indels 100.0%; Score 2211; DB 6; 100.0%; Pred. No. 4.9e-173; tive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 431; Conservative 431 431 DYLINGIYVDI Sequence 431 AA; 61 181 181 241 241 301 301 361 361 421 421 RESULT 15 8888888888888888 ò 용 ò g ò g ò 셤 ò a ò g ð 요 ò 셤

Human secreted/transmembrane protein PRO361. ABU64930 standard; protein; 431 AA (first entry) 15-MAY-2003 ABU64930; ABU64930 

Human, PRO; secreted protein, transmembrane protein; Cornelia de Lange syndrome; gene therapy; immune disorder; inflammatory disease; organ fallure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; cardiac injury; AIDS; cancer; diabetic complication.

US2002173463-A1. Homo sapiens

31-AUG-2001; 2001US-00944944. 21-NOV-2002

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970S-0069378P
970S-0069314P
970S-0069425P
970S-0069664P
970S-00696702P
970S-0069702P
970S-0069702P
970S-006970P
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970S-006970P
980S-0070440P
980S-0070440P
980S-0070692P
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2000WO-US032678
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Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E; Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL; Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;

WPI; 2003-311003/30. N-PSDB; ABX96832.

New transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.

Claim 12; Fig 32; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/
transmembrane polypeptide (designated as PRO proteins). 15 PRO
polypeptides and their encoding polymuclectides are disclosed. Also
conjuded are a vector comprising the PRO uncleic acid, a host cell
included are a vector. a process for producing a PRO polypeptide (by
conjuded are a vector, a process for producing a PRO polypeptide (by
conjuded and recovering the PRO polypeptide (by
conjuded polypeptides, and reast 80% amino acid sequence identity to
isolated polypeptides, a chimaeric molecule comprising PRO fused to a
che PRO polypeptides, a chimaeric molecule comprising PRO fused to a
cherologous amino acid sequence are useful as hybridisation probes,
to PRO. The PRO nucleotide sequence are useful as hybridisation probes,
con chromosome and gene mapping, in generating sense and antisense RNA or
CDNA, in generating transgenic or knock-out animals which can be used in
conformed and screening of therapeutically useful reagents, and in
conformed also be used for chromosome identification, and tissue typing
conformed and screening of the PRO polypeptides and nucleic
conformatified as chordin) is a candidate gene for Cornelia de Lange
Syndrome. Other PRO proteins are variously implicated in immune
conformed the proporteins are variously implicated in immune
conformed the proportein sease, organ failure, atherosclarosis, cardiac
injury, infertility, birth defects, premature aging, cardiac injury,

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                                                                                                                                                                                                                                                 TDPPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                       TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                                                                                                                                                                                                                                                                                                                                                                                                                              AVLTITEQAPIDSKGSLETIPFIEISNLILNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
                                                                                                                                                                                         BDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
                                                                                                                                                              9
AIDS, cancer and diabetic complications. The present sequence represents a PRO protein
                                                                                                                                                1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ
                                                                                                                               1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ
                                                                                                                                                                                                                                                                                                             181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
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                                                                        Length 431;
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                                                                      100.0%; Score 2211; DB 6;
100.0%; Pred. No. 4.9e-173;
ive 0; Mismatches 0;
                                                                                                Matches 431; Conservative
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Best Local Similarity
                                           Sequence 431 AA;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Kljavin, Ivar
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548PB.Cl
CURRENT APPLICATION WHERE: US/09/866,028
CURRENT PILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 83
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US-09-134-001C-4463
US-09-218-095A-1
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US-09-248-766A-11
US-09-248-766A-11
US-09-928-361B-18
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100.0%; Pred. No. 2.9e-202;
tive 0; Mismatches 0;
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
Roy, Margaret
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Best Local Similarity 100.
Matches 431; Conservative
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-83
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APPLICANT: TUMAS, DANIEL
APPLICANT: TUMAS, DANIEL
APPLICANT: WOOG, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE DETERRENCE: PESS48PLT.
CURRENT APPLICATION NUMBER: 105/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR PELING DATE: 2001-09-26
PRIOR PELING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/065,334
PRIOR PELING DATE: December 1, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR PLING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PLING DATE: December 11, 1997
PRIOR PLING DATE: December 12, 1997
PRIOR PLING DATE: December 12, 1997
PRIOR PLING DATE: December 12, 1997
PRIOR PLING DATE: December 16, 1997
PRIOR PLING DATE: December 17, 1997
PRIOR PLING DATE: December 17, 1997
PRIOR PPLICATION NUMBER: 60/069,694
PRIOR PLING DATE: December 17, 1997
PRIOR PPLING DATE: December 17, 1997
PRIOR PPLING DATE: December 17, 1997
PRIOR PLING DATE: December 18, 1997
PRIOR PLING DATE: DECEMBER: 60/069,017
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Patent No. 6734288
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
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APPLICANT: Botstein, David
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100.0%; Pred. No. 2.9e-202;
tive 0; Mismatches 0;
                                                         PRIOR FILING DATE: February 9, 1998
PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: Pebruary 25, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: September 16, 1998
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PRIOR PILING DATE: December 1, 1998
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PRIOR PILING DATE: OF 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 16, 1999
PRIOR PILING DATE: NOW 6734288ember 30, 1999
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PRIOR PILING DATE: Pecember 16, 1999
PRIOR PILING DATE: PECTUARY 21, 2000
PRIOR PILING DATE: PEDRUARY 12, 2000
PRIOR PILING DATE: PEDRUARY 12, 2000
PRIOR PILING DATE: MARCH 2, 2000
PRIOR PILING DATE: PEDRUARY 12, 2000
PRIOR PILING DATE: PEDRUARY 12,
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PLICATION NUMBER: 60/074,092
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Matches 431; Conservative
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; ORGANISM: Homo Sapien
US-09-944-457-83
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276 SOPPITLIS-----TVPTRAAATLQAMATTAVLITTFQAPTDSKGSLETIPFT 323
                                                 158 TDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAH 217
                                                                                                                                                 LLPENVSALPATVAVASPHT----TSATPKPATL-LPTNASV----TPS--GTSQPQLA 265
                                                                                                                                                                             | :| || :| || || || || SAP-TTAASSTPMTLALPAPTSTXTGRTPSTTATGHPSLS 113
                                                                                                                                                                                                                                                 TTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQA-PTDSKGSLETIPFTE 324
                                                                                                                                                                                                                                                                                  325 ISNLTLNTGNVYNPTA---LSMSNVESSTMNKTASWEGREASPGSSSOGSVPENOYGLPF 381
                                                                                                                                                                                                                                                                                                                                                                                                  170 VPPMX-----PQAQGPISQVSVDQPVVNTT------XKSTXMPSNTTXEPL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giot. Loic
APPLICANT: Giot. Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: 08/10/329
CURRENT FILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR PILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURPARESEGFORMATTER VERSION 0.9
SOFTWARE: CURPARESEGFORMATTER VERSION 0.9
                                                                                  220 PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 TQAVVDKTLLLVVLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLINGMYAD 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 ----EKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 149.5; DB 4; Length 5179; 34.1%; Pred. No. 0.00095; ive 12; Mismatches 52; Indels 19;
Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (0)...(0)
COTHER INFORMATION: Polypeptide Accession Number Q02817
US-09-538-092-1258
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Patent No. 6350859
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1258, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 34.1%
Matches 43; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1628 PPTSTT 1633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-538-092-1258
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80;
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                                                                                                                                                                                                                                                 266
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  Matches
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-489-847-332
                                                                                                                            241 TPKPATLLEPINASVIPSGTSQPQLATTAPPVITVTSQPPTILISIVFTRAAATLQAMATT 300
                                                                                                                                                                                                                              301 AVLTTFPQAPTDSKGSLETIPFTEISNITLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360
                                                                                                                                                                                                                                                                                                                              361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equals any of the naturally occurring L-amino acids
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HLEKLPKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                            181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                                                                                                                                                                                                                                                                  361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL
                                                                                                                                                                                                  301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTWNKTASWEGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: US/09/489,17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER PLICATION NUMBER: 60/095,486

EARLIER PELING DATE: 1998-08-05

EARLIER PELING DATE: 1998-08-05

EARLIER PELING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/095,454

EARLIER APPLICATION NUMBER: 60/095,454

EARLIER PILING DATE: 1998-08-06

EARLIER PILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
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SEQ ID NO 332
                                                                                                                                                                                                                                                                                                                                                                                                    421 DYLINGIYVDI 431
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
LOCATION: (195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SITE
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181
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NAME/KEY: Modified-site
LOCATION: 338..381
OTHER INFORMATION: /note
                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                 represent a putative TM
                                                                                                                                                                                                                                                                                                                                    LOCATION: 544..564
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 565..629
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                        NAME/KEY:
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LOCATION: 1..629
OTHER INFORMATION: /Function = "Amino acid sequence for the
Drosophila Melanogaster Scavenger Receptor
Class CI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
LOCATION: 21..74
OOTHER INFORMATION: /note= "Amino acids 21-74 represent
complement control protein domain
number 1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Disulfide-bond
LOCATION: 22..381
OTHER INFORMATION: /note= "The cysteines at positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "Amino acids 1-20 represent a putative signal sequence."
TITLE OF INVENTION: Class BI and CI Scavenger Receptors NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPES FLOPPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/241,581B

FILING DATE: 02-P6-1999

CLASSIFICATION: CURROWN:

MAME: Paber: Patent L.

NAME: Paber: Patent L.

NAME: PABER: Patent L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: MIT6620

TELEFAXION INFORMATION:

TELEFAX: (404) 873-8794

INFORMATION: POR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "Positions 30-32, 90-92, 129-131, 180-182, 253-255 and 351-353 represent potential N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Amino acids 128-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Amino acids 75-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: 75..127

OTHER INFORMATION: note= "Amino aci represent complement control protein domain number 2."
                                                            ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
LOCATION: 128..312
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent an MAM domain."
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LOCATION: 30.353
OTHER INFORMATION: /note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
                                                                                                                                               STATE: Georgia
COUNTRY: USA
                                                                                                                         CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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213 QEIAHLLPENVSALPATVAVASPHT-----TSATPKPATLLPTNASVTPSGTSQ 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
LOCATION: 578..592
OTHER INFORMATION: /note= "Amino acids 578-580 and
590-592 represent protein kinase C
sites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 576..602
OTHER INFORMATION: /note= "Amino acids 576-579 and 07HER INFORMATION: /note= "Amino acids 576-579 and sites."
22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216, 217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381 represent potential disulfide linkages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
LOCATION: 596..599
OTHER INFORMATION: /note= "Amino acids 596-599
represent a CAMP protein kinase site."
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                LOCATION: 387..514
OTHER INFORMATION: /note= "Amino acids 387-514 represent a mucin-like potential O-linked glycosylation region."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acids 544-565
TM domain."
                                                                                                                                                                  OTHER INFORMATION: /note= "Amino acids 338-381 represent a somatomedin B domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 565-629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.6%; Score 145.5; DB 3; Best Local Similarity 22.9%; Pred. No. 7.6e-05; Matches 48; Conservative 30; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class BI Scavenger Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent a putative cytoplasmic domain."
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APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Sca
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:| : | | | : | | | | 383 KELLTTEDDISSLPPTVTSTTTRKSTTTTTSTTTTKRPTTTTTKATT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 QEIAHLLPENVSALPATVAVASPHT-----TSATPKPATLLPTNASVTPSGTSQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 PQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 FTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASW-----EGREASPGSSSQGSVPE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY: Modified-site
LOCATION: 576..602
OTHER INFORMATION: /note= "Amino acids 576-579 and
OTHER INFORMATION: 599-602 represent casein kinase II sites."
PERTURE:
NAME/KEY: Modified-site
LOCATION: 578..592
OTHER INFORMATION: 70.0te= "Amino acids 578-580 and
OTHER INFORMATION: 590-592 represent protein kinase C sites."
                                                                                                                                    /note= "Amino acids 387-514 represent a mucin-like potential O-linked glycosylation region."
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Domain
LOCATION: 565..629
OTHER INFORMATION: /note= "Amino acids 565-629
OTHER INFORMATION: represent a putative cytoplasmic domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 KRITTÍTKKÞITÍTSÍTPKÞÍTITSÍTPKSITSÍTSÍTSÍTPTTÍTÍTINVFÍTKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 145.5; DB 4; Length 629; 22.9%; Pred. No. 7.6e-05; Live 30; Mismatches 79; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Amino acids 596-599 represent a CAMP protein kinase site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application PC/TUS9507721
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
ATITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
                               represent a somatomedin B domain.
                                                                                                                                                                                                                 NAME/KBY: Domain
LOCATION: 544..564
OTHER INFORMATION: /note= "Amino acids 544-565
OTHER INFORMATION: represent a putative TM domain.
FEATURE:
          OTHER INFORMATION: /note= "Amino acids 338-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|::|:||:
-----VLYLLLGIVLV 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                          NAME/KEY: Modified-site
LOCATION: 387.514
OTHER INFORMATION: /note=
OTHER INFORMATION: glycosy
FRATURE:
NAME/KEY: Domain
LOCATION: 544.564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.99
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 596.599
CTHER INFORMATION:
CTHER INFORMATION:
US-08-265-428-6
                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
PCT-US95-07721-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc. feature
LOCATION: 1..629
OTHER INFORMATION: /Function = "Amino acid sequence for the Drosophila Melanogae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=""The cysteines at positions 22, 45, 59, 72, 77, 99, 113, 125, 136, 144, 216, 217, 254, 310, 339, 343, 361, 363, 367, 373, 374 and 381 represent potential disulfide linkages."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Amino acids 75-127
represent complement control protein domain number
2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 30.353
OTHER INFORMATION: /note= "Positions 30-32, 90-92,
OTHER INFORMATION: 129-131, 180-182, 253-255 and 351-353 represent
OTHER INFORMATION: potential N-glycosylation sites."
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Amino acids 21-74 represent complement control protein domain number 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: .1..20
OTHER INFORMATION: /note= "Amino acids 1-20 represent
OTHER INFORMATION: a putative signal sequence."
                                                                                                                                                                                                                                           MEDIUM TIVEL

COMPUTER: LAMPY WITH

COMPUTER: TANGED

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/265,428

FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGBMT INFORMATION:
NAME: Pabbet, Patrea L.
REGISTRATION NUMBER: MIT6620
TELEPHONE: (404) 815-6598
TELEPHONE: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 128..312
OTHER INFORMATION: /note= "Amino acids 128-312
OTHER INFORMATION: represent an MAM domain."
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY, modified-site
LOCATION: 21..74
OTHER INFORMATION: complen
FEATURE:
NAME/KEY: Modified-site
LOCATION: 75..127
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
OTHER INFORMATION: 2."
                                                                                                                                                 COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Modified-site
LOCATION: 128.312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Modified-site
LOCATION: 30.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 22.381
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: ERATURE:
NAME/KE: Modified-ELOCATION: 338.381
                                                                                                                                    Georgia
                                                                                                       CITY: Atlanta
STATE: Georgia
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FEATURE:
NAME/KEY: Domain
LOCATION: 544.564
OTHER INFORMATION: /
OTHER INFORMATION: FEATURE:
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OTHER INFORMATION: 7
OTHER INFORMATION: 5
OTHER INFORMATION:
OTHER INFORMATION:
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SEQ ID NO 647
LENGTH: 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAUCE:
NAME/KEY: misc. feature
LOCATION: 1..629
OTHER INFORMATION: Drosophila Melanogaster Scavenger Receptor
THEN INFORMATION: Class CI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Positions 30-32, 90-92, 129-131, 180-182, 253-255 and 351-353 represent potential N-glycosylation sites."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Amino acids 21-74 represent complement control protein domain number 1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "PEATURE:
NAME/KEY: Modified-site
LOCATION: 338..381 / note= "Amino acids 338-381
OTHER INFORMATION: represent a somatomedin B domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Amino acids 1-20 represent
a putative signal sequence."
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NAME/KEY:
NOALfied-site
LOCATION:
OTHER INFORMATION:
NAME/KEY:
NAME/KEY:
OTHER INFORMATION:
OTHER I
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "RATURE:
NAME/KEY: Modified-site
LOCATION: 387..514
OTHER INFORMATION: /note= "Amino acids 387-514
                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 629 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 22.381
OTHER INFORMATION: 22, 45,
OTHER INFORMATION: 22, 45,
OTHER INFORMATION: 217, 25
OTHER INFORMATION: and 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
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383 KELLITTEDDISSLPPTVISISITRKSTITITISTITITRKPITITIKATIT 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 POLATTAPPVITVISOPPTILISTVFTRAAATLOAMATTAVLTTTFQAPTDSKGSLETIP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 FTEISNLTLNTGNVYNPTALSMSNVESSTWNKTASW-----EGREASPGSSSQGSVPE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-54
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR PAPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site

| NAME/KEY: Modified-site

| LOCATION: 596..599

| OTHER INFORMATION: /note= "Amino acids 596-599

| OTHER INFORMATION: represent a cAMP protein kinase site."

PCT-US95-07721-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amino acids 578-580 and 590-592 represent protein kinase C sites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 II
                                                                                                                                                                                                                                                                /note= "Amino acids 565-629 represent a putative cytoplasmic domain."
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Amino acids 576-579 and 599-602 represent casein kinase sites."
represent a mucin-like potential O-linked glycosylation region."
                                                                                                                                 /note= "Amino acids 544-565 represent a putative TM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6%; Score 145.5; DB 5; Best Local Similarity 22.9%; Pred. No. 7.6e-05; Matches 48; Conservative 30; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 NOYGLPFEKWLLIGSLLFGVLFLVIGLVLL 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 647, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
                                                                                                                                                                                                            NAME/KEY: Domain
LOCATION: 565.229
COTHER INFORMATION: repress
OTHER INFORMATION: repress
OTHER INFORMATION: domain
FEATURE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 576..602
OTHER INFORMATION: /note=
OTHER INFORMATION: 6599.60
OTHER INFORMATION: sites.
FRAVURE:
NAME/KEY: Modified-site
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APPLICANT: Sternberg, Paul W.
APPLICANT: Barr, Maureen M.
TITLE OF INVENTION: BRHAVIOR IN NEWATODES AND ASSAYS BASED THEREON
FILE REFERENCE: 18021-2901B
CURRENT APPLICATION NUMBER: US/09/479,467A
CURRENT PILING DATE: 2000-01-06
PRIOR FILING DATE: 1999-01-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEPSTSTITIEVISISSIVITIEPITILITISTAST-----STIEPSTSTVITSPST 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 TLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 SPVTSTVTSSSSSSTTVTTPTSTESTSTSPSSTVTTSTTAPSTSTTGPSSSSSTPSSTAS 515
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Sequence 712, Application US/09538092

Fatent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

APPLICANT: Giot, Loic

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT APPLICATION NUMBER: 60/127,352

FRIOR FILING DATE: 1999-04-01

FRIOR APPLICATION NUMBER: 60/178,965

FRIOR PILING DATE: 2000-02-01

FRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 ENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 136; DB 4; Length 3178; 23.6%; Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 133; DB 4; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (0)...(0) ; OTHER INFORMATION: Polypeptide Accession Number YOL105C US-09-538-092-712
                                                                     516 SSVSSTASSTQSSTSTQQSSTTTKSETTTSSDGTNPD 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 SSVSSTASSTQSSTSTQQSSTTTKSETTTSSDGTNPD 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSMSNVESSTMNKTASWEG---REASPGSSSQGSVPE 374
                                   341 LSMSNVESSTMNKTASWEG---REASPGSSSQGSVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38; Mismatches
                                                                                                                                                                                                    Sequence 4, Application US/09479467A Patent No. 6723557 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: C. Elegans Lov-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-538-092-712
                                                                                                                                                      RESULT 10
US-09-479-467A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-479-467A-4
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LENGTH: 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
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APPLICANT: Sternberg, Paul W.
APPLICANT: Barr, Maureen M.
APPLICANT: Barr, Maureen M.
POLYCYSTIC KIDNEY DISEASE GENE HOMOLOGS REQUIRED FOR MALE MAT
TITLE OF INVENTION: DEMANIOR IN NEWATODES AND ASSAYS BASED THEREON
FILE REFERENCE: 18021-2901B
FILE REFERENCE: 18021-2901B
FILE REPERENCE: 2000-1-06
PRIOR APPLICATION NUMBER: 06/115,127
PRIOR APPLICATION NUMBER: 60/115,127
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PARCELIN VEY: 2.00
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                                                                                                                                                                                                                                                                                                                               510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 ASPLPSVWSDITSSEASSISSNLASSSAPSDNNSTIASASLIVT----KTKNSVVSSIV 618
                                                                                                                                                                                                                                                                                                                                                                                                            59 TQEDCINSCCSTKN-----ISGDKACNLMIFDTRKT-ARQPNCYLFFCPNEEACP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 LKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDIS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 WRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQ------FSSDQEI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 SSITSSETTNESN-----LATSSTSLLSNKATARSLSTSNATSASNVPTGTFSSMSSH 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AHLLPENVSALPATVAVASP------HITSATPKPATLLPINASVIPSGTSQPQL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 ATTAPPVITVISQPPTILISTVFTRAAATLQAM-----ATTAVLITTFQAPTDSKG 315
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                                                                                                                                                                                                                                                                                                        1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVID--IQSSLSKGIRGNEPVYTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 ENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 6.2%; Score 136; DB 4; Length 2870;
11 Similarity 23.6%; Pred. No. 0.0071;
37; Conservative 38; Mismatches 70; Indels 12; Gaps
                                                                                                                                                                                                                              87;
                                                                                                                                                                             Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 SLETIPFIEISNLTLNTGNVYNP-----TALSMSNVESSTWNKT 354
                                                                                                                                                                                                                           Indels
                                                                  ; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR317W
US-09-538-092-647
                                                                                                                                                                        Query Match 6.5%; Score 144.5; DB 4; Best Local Similarity 21.2%; Pred. No. 0.00025; Matches 86; Conservative 63; Mismatches 169;
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ORGANISM: C. Elegans Lóv-1 sy582 deletion protein
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     cerevisiae
ORGANISM: Saccharomyces
                         FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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SEQ ID NO 15
LENGTH: 2870
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ORIGINAL SOURCE:
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                                                                                             284 STVFTRAAATLQAMATTAVLT------TTFQAPTDS-----KGSLETI 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                     360 ATAAASNNRSNSTSKQRLSGGAIAGIVIGVVFGVIFII--LILLEFLIWR---RRKSHDQL 414
                                                                164 IDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV 223
                                                                                                                                                    224 SALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
                                                                                                                                                                                                                                                                                                                          321 PFTEISNLTLNTG-----NVYNPTALSMSNVESSTWNKTASWEGREASPGSS 367
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3. Application US/09294663
Sequence 10. 6765127
GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6765127e1 Invertebrate Intestinal Mucin
TITLE OF INVENTION: AND and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6765127th Tioga Street
                          62;
Best Local Similarity 22.6%; Pred. No. 0.00097;
Matches 68; Conservative 57; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BII-39-CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: (607) 256-200
TELEPRONE: (607) 256-3628
INFORMATION FOR SEQ IN NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/103,429
FILING DATE: 24-UN-1998
ATTORNEY/AGENT INFORMATION:
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19-APR-1999
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Ithaca
STATE: NY
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220 PENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPP 279
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                                                                                                                                                                                                                                                                                                                          280 TILISTVETRA-AATLOAMATTAVLTITFOAPTDSKGSLETIPFTEISNLTLNTGNVYNP 338
                                                                                                        Query Match 6.0%; Score 132; DB 4; Length 788; Best Local Similarity 31.0%; Pred. No. 0.0021; Matches 48; Conservative 15; Mismatches 78; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09294663

Patent No. 6763127
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Grandos, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6765127el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6765127th Tioga Street
CITY: Ithaca
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CUBRENT APPLICATION DATA:
PLILOATION NUMBER: US/09/294,663
FILING DATE: 19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                339 TALSMSNVESSTMNKTASWEGREASPGSSSOGSVP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AATTPAATTPAATT-----TPGVPAPTSAP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-39-CIP
ORGANISM: Trichoplusia ni
TISSUE TYPE: peritrophic membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/103,429
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Trichoplusia ni
; TISSUE TYPE: peritrophic membrane
US-09-294-663-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (607) 256-3628
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 807 amino acids
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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Ithan STATE: NY
                                                       US-09-294-663-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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385 Sherman Avenue, Suite 6

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APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: WITH SECOND S
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                                                                                                                                                                                                PAETTQAPAT--TQAPITTQA-PITTTQAPITTTQAPITTTQAPITTQAP---TTTQAPI 149
                                                                                                                         220 PENVSALPATVAVASPHTISATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPP 279
                                                                                                                                                                                                                                                                                        280 TTLISTVFTRA-AATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNP 338
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                                              Indels
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    31.0%; Pred. No. 0.0022;
tive 15; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 TALSMSNVESSTMNKTASWEGREASPGSSSQGSVP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 AATTPAATTPAATTPAAT-----TPGVPAPTSAP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PETERS, VERNY, JONES & BIKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08700651B Patent No. 6015882
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Patent No. 6071518
GENERAL INFORMATION:
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                                         Conservative
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SEQ 1D NO 12
LENGTH: 175
TYPE: PRT
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TITLE OF INVENTION: PEP
TITLE OF INVENTION: THE.
TITLE OF INVENTION: FOR
TITLE OF INVENTION: SPE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VEI
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Best Local Similarity
Matches 48; Conserv
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286 VFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSN 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 LPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLIST
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0.00036;
ches 74; Indels
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129; DB Pred, No. 0.000
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
PILING DATE: 13-8EP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                        CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 26, 2005, 21:53:37 Job time : 57 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
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Best Local Similarity 27.3*
Matches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                            ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Palo Alto
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                                          USA
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                                          COUNTRY:
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April 26, 2005, 21:53:41 ; Search time 1465 Seconds (without alignments) 97.906 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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DB seq length: 200000000
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Perfect score:
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Maximum I
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		Appl	App	App	App	App	Appl	App	Appl	Appl	App	App	Appl	App
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		US-09-866-028-83	US-09-989-722-515	19-989-723-51	19-989-219-51	19-989-727-51	9-944-449-83	19-989-731-51	9-944-457-83	9-944-862-83	9-989-732-51	9-991-073-51	19-945-587-83	JS-09-990-442-515
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	Query Match Length DB	431	431	431	431	431	431	431	431	431	431	431	431	431
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100.0%; Score 2211; DB 9; Length 431; 100.0%; Pred. No. 2.1e-172;

TYPE: PRT
CORGANISM: Homo Sapien
US-09-866-028-83

Query Match Best Local Similarity

Sequence 81, Apple Sequence 83, Apple Sequence 81, Apple Sequence 815, Apple Sequence 815, Apple Sequence 81, Apple Sequence 81, Apple Sequence 81, Apple Sequence 81, Apple Sequence 81, Apple Sequence 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815, Apple 815,	POLYPEPTIDES AND NUCLEIC
US-09-991-163-515 US-09-945-011-83 US-09-944-366-83 US-09-944-412-83 US-09-944-412-83 US-09-944-412-83 US-09-944-412-83 US-09-944-413-83 US-09-944-614-83 US-09-944-614-83 US-09-944-614-83 US-09-944-944-83 US-09-944-944-83 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-181-515 US-09-991-681-515 US-09-991-781-515	ALIGNMENTS 56028 327 327 327 327 328 328 329 329 329 329 329 329
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PRIOR APPLICATION NUMBER: 60/088742
PRIOR PELLING DATE: 1998-06-10
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PRIOR PELLING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08824
PRIOR PILING DATE: 1998-06-10
PRIOR PELLING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08858
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08861
PRIOR FILING DATE: 1998-06-11
PRIOR PELLING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR PAPLICATION NUMBER: 60/08876
PRIOR PILING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
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PRIOR PELLING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-04
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PRIOR PLING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088167
PRIOR APPLICATION NUMBER: 60/088120
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
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REPLIED DATE: 1998-06-02
REPLIED DATE: 1998-06-02
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REPLIED DATE: 1998-06-03
REPLIED DATE: 1998-06-03
REPLIED DATE: 1998-06-03
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FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
APPLICATE: 1998-06-05
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088742
                                                                                                           FILING DATE: 1997-11-24
APPLICATION UNMBER: 60/075945
APLICATE 1998-02-25
APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
                                                              FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/083322
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                                      APPLICATION NUMBER: 60/065311
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                                                                                                                                                                                                                                 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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                                           1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLXKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
                                                                                      1 MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 60
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
  Gaps
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CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
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Patent No. US20020072067A1
GENERAL INPERMATION:
APPLICANT: Ashkenazi, Avi J.
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Grimaldi,J.Christopher
Gurney,Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Napier, Mary A.
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    Matches 431; Conservative
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Eaton, Dan L.
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US-09-989-722-515
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R FILING DATE: 1998-06-18
R APPLICATION NUMBER: 60/089907
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                APPLICATION NUMBER: 60/089532
FILING DAFE: 1998-06-17
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION UNDHER: 60/090472
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
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APPLICATION UNDBER: 60/090540
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090435
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090678
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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LING DATE: 1998-06-16
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             R APPLICATION NUMBER: 60/091478
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-01
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091633
R FILING DATE: 1998-07-07
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R APPLICATION NUMBER: 60/09192
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Patent No. US20020072092A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Ferrara, Napoleone
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Gerber, Hanspeter
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Goddard, Audrey
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Botstein, David
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PPLICATION NUMBER: 60/090435
ILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/088810
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APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/08826
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/089440
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LICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089600
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FILING DATE: 1998-06-11
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IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG2
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
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OR FILING DATE: 1997-06-16

OR APPLICATION NUMBER: 60/062250

OR APPLICATION NUMBER: 60/065186

OR APPLICATION NUMBER: 60/065118

OR FILING DATE: 1997-11-12

OR APPLICATION NUMBER: 60/065311

OR PILING DATE: 1997-11-13

OR APPLICATION NUMBER: 60/066770

OR PILING DATE: 1997-11-24
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IG DATE: 1998-06-03
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APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-10
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PLICATION NUMBER: 60/084600
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                                                                                                                         Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                                                    Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy I
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                    lapier, Mary A.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PIC56
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PLING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PLING DATE: 1998-04-28
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PRIOR APPLICATION NUMBER: 60/08767
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PRIOR APPLICATION NUMBER: 60/08025
PRIOR PLING DATE: 1998-06-03
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PRIOR APPLICATION NUMBER: 60/08026
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PRIOR PRIOR DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/08025
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PRIOR APPLICATION NUMBER: 60/08026
                                                                                                       US-09-989-279-515; Application US/09989279; Sequence 515, Application US/09989279; Patent No. US20020072496A1; GENERAL INPORMATION: APPLICANT: ABhkenazi, Avi J.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Gerritsen, Mary E
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Botstein, David
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Eaton, Dan L.
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361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
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CURRENT APPLICATION NUMBER: 2001-09-26
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PRIOR FILING DATE: 1988-07-02
PRIOR APPLICATION NUMBER: 60/09198
PRIOR FILING DATE: 1988-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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PRIOR APPLICATION NUMBER: 09/866,028
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Patent No. US20020102647A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Conservative 0;
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Filvaroff, Ellen
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Tumas, Daniel
Wood, William
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Napier, Mary
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61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
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Pred. No. 2.1e-172;
; Mismatches 0;
  PRIOR APPLICATION NUMBER: PCT/USO1/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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Patent No. US20020103125A1
GENERAL INFORMATION:
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tive 0;
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Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Ferrara, Napoleone
Fong, Sherman
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Roy, Margaret Ann
Stewart, Timothy A
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Goddard, Audrey
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Best Local Similarity 100.
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Botstein, David
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                                                                                                                 TYPE: PRT
CORGANISM: Homo Sapien
US-09-944-449-83
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                                                                      SEQ ID NO 83
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OR APPLICATION NUMBER: PCT/US99/12252
OR APPLICATION NUMBER: PCT/US99/12090
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: No. US20020102647Atember 30, 1999
OR FILING DATE: No. US20020102647Atember 30, 1999
OR FILING DATE: No. US20020102647Atember 30, 1999
OR FILING DATE: PCT/US99/28313
                                                                                                     PRIOR APPLICATION NUMBER: 60/069335
PRIOR APPLICATION NUMBER: 60/069325
PRIOR APPLICATION NUMBER: 60/069325
PRIOR APPLICATION NUMBER: 60/069425
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 16, 1997
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                                                                                       FILING DATE: December 11, 1997
APPLICATION WINBER: 60/066335
FILING DATE: December 1, 1997
APPLICATION NUMBER: 60/069,278
                                         FILING DATE: December 3, 1997
APPLICATION NUMBER: 60/069,334
                        APPLICATION NUMBER: 60/067,41
2001-05-25
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APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090435
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NG DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
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APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090557
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/089514
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089599
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
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                         PLICATION NUMBER: 60/088861
LING DATE: 1998-06-11
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APPLICATION NUMBER: 60/089801
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APPLICATION NUMBER: 60/089907
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     PPLICANT: Zhang, Zemin
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
ILE REFERENCE: P2730P1C70
                                                                       CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
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PRIOR PRILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06531
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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R APPLICATION NUMBER: 60/087607

R FILING DATE: 1998-06-02

R APPLICATION NUMBER: 60/087609

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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
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PPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088028
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APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: 05/06/944,457
CURRENT PELING DATE: 2001-09-26
FRIOR PELING DATE: 2001-09-26
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FRIOR PELING DATE: DECEMBER 3,1997
PRIOR APPLICATION NUMBER: 60/06/334
PRIOR FILING DATE: DECEMBER 11,1997
PRIOR APPLICATION NUMBER: 60/06/9,234
PRIOR FILING DATE: DECEMBER 11,1997
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PRIOR PELING DATE: DECEMBER 11,1997
PRIOR PELING DATE: DECEMBER 11,1997
PRIOR APPLICATION NUMBER: 60/06/9,425
PRIOR APPLICATION NUMBER: 60/06/9,425
PRIOR APPLICATION NUMBER: 60/06/9,696
PRIOR FILING DATE: DECEMBER 16,1997
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         Botstein, David
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Goddard, Audrey
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                                                 PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR PILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09
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; Sequence 83, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 431; Conservative
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Hillan, Kenneth
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PRIOR FILING DATE: No. US20020110859Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/14042
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PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: March 2, 2000
PRIOR PRILING DATE: March 30, 2000
PRIOR PRILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR PRILING DATE: DECEMBER: PCT/US00/36520
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US-09-944-862-83
; Sequence 83, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
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PRIOR FILING DATE: NO. US20020115145Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
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PRIOR PILING DATE: December1, 1999
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PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PCT/US00/03565
PRIOR APPLICATION NUMBER: PCT/US00/03656
PRIOR PILING DATE: PEDRUARY 11, 2000
PRIOR PILING DATE: PEDRUARY 22, 2000
PRIOR FILING DATE: PCT/US00/05841
PRIOR PILING DATE: PATOR NUMBER: PCT/US00/06439
PRIOR FILING DATE: MARCh 2, 2000
PRIOR FILING DATE: MARCh 30, 2000
PRIOR FILING DATE: MARCh 30, 2000
PRIOR PILING DATE: MARCh 32, 2000
PRIOR PILING DATE: MARCh 32, 2000
PRIOR PILING DATE: MARCh 32, 2000
PRIOR PILING DATE: MARCH 32, 2000
PRIOR APPLICATION NUMBER: PCT/US00/12678
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PRIOR FILING DATE: PEDRUARY 28, 2001
PRIOR FILING DATE: PEDRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
LENGTH 431
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Sequence 515, Application US/09989732 Patent No. US20020123463A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.

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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088876
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APPLICATION NUMBER: 60/088734
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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CURRENT APPLICATION NUMBER: US/09/991,073
CURRENT FILING DATE: 2001-11-14
PRIOR PELLORATION NUMBER: 60/049787
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Patent No. US20020127576A1
GENERAL INFORMATION:
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Goddard, Audrey
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Botstein, David
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R APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090694 FILLING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 PILLING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/09044 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 LICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090472 ILING DATE: 1998-06-24 PPLICATION NUMBER: 60/090557 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 LICATION NUMBER: 60/090431 FILING DATE: 1998-06-22 LING DATE: 1998-06-24 LING DATE: 1998-06-24 LING DATE: 1998-06-24 FILING DATE: 1998-06-24 FILING DATE: 1998-06-2 FILING DATE: 1998-06-PRIOR
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P5548PLC1: CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
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PRIOR PILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/069,278 ö 180 240 240 300 360 361 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRL 420 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120 180 241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVITVTSQPPTTLISTVFTRAAATLQAMATT 300 301 AVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGR 360 EASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLULGRILSESLRRKRYSRL 420 9 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 1 MFPGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ 181 HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 301 AVLTTTPOAPTDSKGSLETIPFTEISNLTINTGNVYNPTALSMSNVESSTMNKTASWEGR MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ Gaps ; 0 Indels , Pred. No. 2.1e-172; 0; Mismatches 0; Sequence 83, Application US/09945587 Patent No. US20020127643A1 GENERAL INFORMATION: Grimaldi, Christopher 100.08; Ferrara, Napoleone Filvaroff, Ellen APPLICANT: Baker, Kevin APPLICANT: Botstein, David APPLICANT: Eaton, Dan DYLINGIYVDI 431 Gerritsen, Mary Goddard, Audrey Gurney, Austin Godowski, Paul Roy, Margaret Tumas, Daniel Wood, William Kljavin, Ivar Napier, Mary DYLINGIYVDI

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                                                                                      1 MFFGGEGSLIYTLVIICFLILRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQ
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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ive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-11-14
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Patent No. US20020132252A1
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 100.
Matches 431; Conservative
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APPLICANT: Ashkenazi, Avi J
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Eaton, Dan L.
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Tumas, Daniel
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CURRENT PARLICATION NUMBER: 60/140978

PRIOR PRILING DATE: 1997-06-116

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PRIOR PRILING DATE: 1997-11-112

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        Grimaldi, J. Christopher
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                    Gurney, Austin L.
Kljavin, Ivar J.
                                                                                        Napier, Mary A.
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Patent No. US2002013253A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Betein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Faton, Dan L.
APPLICANT: Fong. Sherman
APPLICANT: Gerber, Hanspeter
                                             PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091549
PRIOR PILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/09163
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09198
PRIOR PILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/09192
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Gerber, Hanspeter
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        R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R APPLICATION NUMBER: 60/08810
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R APPLICATION NUMBER: 66/089600

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R APPLICATION NUMBER: 66/089653
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R APPLICATION NUMBER: 60/088858
R FILING DATE: 1998-06-11
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090431
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FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/08940
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/08826
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PRIOR PELING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
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PRIOR PILING DATE: 1998-06-25
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Best Local Similarity 100.0%;
Matches 431; Conservative 0; 121 301 301 361 241 361 셤 ò g ò ద g 셤 셤 ò ò ò ò

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                                          OR FILING DATE: December 16, 1998

OR APPLICATION NUMBER: 09/216, 157

OR FILING DATE: December 22, 1998

OR APPLICATION NUMBER: 09/254, 31

OR FILING DATE: March 3, 1999

OR APPLICATION NUMBER: PCT/US99/21090

OR RILING DATE: September 15, 1999

OR APPLICATION NUMBER: PCT/US99/21409

OR RAPLICATION NUMBER: PCT/US99/21409

OR RAPLICATION NUMBER: PCT/US99/28409

OR RAPLICATION NUMBER: PCT/US99/28409

OR RILING DATE: No. US20020132768Alember 30, 1999

OR RILING DATE: December 11, 1999

OR RILING DATE: December 11, 1999

OR RAPLICATION NUMBER: PCT/US99/28301

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100.0%; Pred. No. 2.1e-172;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR PLING DATE: Warch 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: June 22, 1999
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PRIOR FILING DATE: September 15, 1999
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PRIOR PILING DATE: July 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
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Matches 431; Conservative
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; ORGANISM: Homo Sapien
US-09-945-015-83
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ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT PEPLICATION NUMBER: US/99/945,015
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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Patent No. US20020132768A1
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff,Ellen
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
          DYLINGIYVDI 431
                                                    421 DYLINGIYVDI 431
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US-09-945-015-83
          421
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APPLICANT:
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Search completed: April 26, 2005, 22:25:34 Job time : 1467 secs

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Run on:

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US-10-735-014-83 2211 Title: Perfect score:

1 MFFGGEGSLTYTLVIICFLT......LRRKRYSRLDYLINGIYVDI 431 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	hypothetical prote	_			- 12	'n	glycoprotein X pre	chitinase (EC 3.2	mucin 2 precursor	mucin MUČ5B, trach	hypothetical prote	Д	mucin FIM-C.1 - Af	serine proteineas	mucin 6, gastric		Pmel 17 protein .	. 0	melanoma antigen h	membrane glycoprot		probable membrane	hypothetical prote		hypothetical prote	LDL receptor 2 pre	ᇁ	gastric mucin (clo	
SUMMARIES	ID	T29634	S53362	T22808	T22696	T39903	T21389	VGBEX1	JC4566	A43932	T45025	T34293	S25345	A45155	A47547	B46629	859310	853871	A48018	A49179	T45462	T45463	S57180	T34369	S24169	T33369	QRXLL2	A53577	147141	
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de	Query Match	7.9	7.3	7.0	7.0	7.0	6.9	6.8	6.8	6.8	٠	6.7	6.7	9.9		6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.2	6.2	6.2	
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	30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	kt_change 09-Jul-2004	à
RESULT 1 T29634 hypothetical protein C12D12.1 - Caenorhabditis elegans	C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T29634	R;Nhan, M.; Hawking, J. submitted to the EMBL Data Library, March 1996 A;Description: The sequence of C. elegans cosmid C12D12 A;Reference number: Z20656

A;Accession: T29634
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-825 «NHA»
A;Cross-references: UNIPROT:Q17921; EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C
A;Experimental source: strain Bristol N2; clone C12D12

A;Map position: X A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1 C;Superfamily: Epstein-Barr virus membrane antigen gp350 C,Genetics: A,Gene: CESP:C12D12.1

17; Gaps Query Match 7.9%; Score 174.5; DB 2; Length 825; Best Local Similarity 23.7%; Pred. No. 0.00064; Matches 93; Conservative 40; Mismatches 144; Indels 115;

36 36 36	124 PSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLE 183 480 PPTIVTVPTTPTPVPTTINTPPANPTTATPTTVGTSKQTNTISPHLS 526 184 KLFKMDEASAQLLAYKEKGHSQSQFSSDQEIAHLLPENVSALPATVAVASPH 236	124 480 184	8 8 S
33	SLTRNLPSQELPQEDSLIHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLE 18:	124	
67	420 PGYHQISLKQQGSYAFFVYGKNKLYSYGYEGGANKPTVVLAPPTTPGPTFYPVTTVSTMS 479	420	
23	89TAROPNCYLFFCPNEEACPLKPAKGLMSYRIITDF 123	89	
61	363 NTPFFTRNANDTIEIYCTVLSCSSITIDGVKIQITDTKVVQKVDDISYYIFVNTIAN 419	363	
<b>.</b>	52 NEPVYTSTOEDCINSCCSTKNISGDKACNLMIFDTRK	25	ò

TISATPKPATLIPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQA 296 584 TTTGSPTTQTTAPVTKPTVPSSTTQ-----TAPPVTTPTSQPPVTTTSLLTTLTTTVPV 638 237 임 ઢ 셤

639 TITVVPSSATVPTTPPTTVTVAATTTSKAPVVTTSPTLAPTSPTKLPTSPSTVGTSP-T 697 297 MAT-----PTDSKGSLETIPFT 323 B

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324 EISNLTLNTGNVYNPTALSMSNVESSTWNKTA 355

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serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39909;
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
aubmitted to the EMBL Data Library, November 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lypothetical protein F55B11.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.0%; Score 154.5; DB 2; Best Local Similarity 26.6%; Pred. No. 0.014; Matches 47; Conservative 26; Mismatches 89;
                                                                                                                                                                                                                                   Query Match 7.0%; Score 155.5; DB 2; Best Local Similarity 32.7%; Pred. No. 0.011; Matches 48; Conservative 16; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-851 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Introns: 49/3; 123/3; 226/1; 282/3; 669/3; 743/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 LNTGNVYNPTALSMSNVESSTMNKTAS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTT---VPPTTTSSTTTTTTTTTTT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Experimental source: clone F55B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: F55B11.3
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                                                                                                                          Mucin 5AC (clone JER47) - human (fragment)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 53362; S71065

R;Gtyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galiegue-Biochem, J. 305, 211-219, 1995

R;Gtyonnet-Duperat, V.; Audie, J.P.; Debailleul, V.; Laine, A.; Buisine, M.P.; Galiegue-Biochem, J. 305, 211-219, 1995

A;Title: Characterization of the human mucin gene MUC5AC: a consensus cysteine-rich doma A;Reference number: S53361; MUID:95126907; PMID:7826332

A;Reference number: S53361; MUID:95126907; PMID:7826332

A;Retaus: mucleic acid sequence not shown

A;Residues: uncleic acid sequence not shown

A;Residues: uncleic acid sequence: clone JBR47

A;Residues: uncleic acid sequence: clone JER47

A;Experimental source: clone JER47

A;Reference number: S71065

A;Reference number: S71065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPEVSIEHLGQVVQCSREEGLVCRNQDQQGPFKMCLNYEVRVLCCETPKGCPVT---ST 131
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hypothetical protein F56H9.1 - Caenorhabditis elegans

hypothetical protein F56H9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Species: T5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T22808

R;Burton, J.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z19618

A;Accession: T22808

A;Accession: T22808

A;Status: preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: S71065.
A,Molecule type: mRNA
A,Residues: 1-211,'8',213-224,'AR',227-259,'S',261-477 <POR>
A,Rossidues: 1-211,'S',213-224,'AR',227-259,'S',261-477 <POR>
A,Experimental source: EMBL: Z34277; NID:9563374; PIDN:CAA84031.1; PID:9563375
A,Experimental source: clone JER47
C,Genetics: A,Gene: GDB:MUCSAC
A,Acrosereferences: GDB:454136; OMIM:158373
A,Nap position: 11p15.5-11p15.5
C,Keywords: glycoprotein; tandem repeat
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698 APANLTTPTTAPVNPT -- SSTTAPTAPVNPTS 727
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A; Residues: 1-770 <WIL>
A; Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A; Experimental source: clone F56H9
C; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Genetics
A; A; Gene: CESP:F56H9.1
A; Map position: 5
A; Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT:017893; EMBL: Z83318; PIDN: CAB05903.1; GSPDB: GN00022; CESP:F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 LPENVSALPATVAVAS-----PHTTSATPKPATILLPTNASVTPSGTSQPQLATTAPPVT 272
                                                                                                                                                                                                                                                                                                                                                        151 TSTTTTTVPPTTTSTTTTTVPAT----TTSTATTTTVPPTTSTTTTTVPPTTTSTTT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22696
R;Ainscough, R.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 LPENVSALPATVAVASPHTISATPKPATILLPINASVT----PSGTSQPQLATTAPPV--
                                                                                                                                                                                                                                                                                                                                                                                                                              272 --TTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLT
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                                                                                                                                                                                                                   Length 770;
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                                                                                                                                                                                                                                                                     Indels
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A; MCCecule type: DNA
A; Residues: 1-797 < TEL.
A; Residues: 1-797 < TEL.
A; Residues: 1-797 < TEL.
A; Cross-references: UNIPROT: P28968; GB: M86664; NID: G330791; PIDN: AAB02506.1; PID: G33086
A; Cross-references: UNIPROT: P28968; GB: M86664; NID: G330791; PIDN: AAB02506.1; PID: G33086
A; Title: The DNA sequence of equine herpesvirus-1.
A; Reference number: A41831; MUID: 92295566; PMID: 1318606
A; Contents: annotation; possible protein-coding frames
A; Note: neither amino acid nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                         283
                                                                                                                                                                                                                                                                                                            -----VQKTRTSEDKPSSSTTVPTSASTSESSTSSP-MAETSSSSTTSQSSPAST-- 314
                                                                                                                                                                                                                                                                                                                                                                                                                    315 STV--PESSTVGSTPTTGLTTLSTNEQSTSTSSGGHSTSTFGTTSE-TPETSTDFTATST 371
                                                                                                                                                               164 TDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENV 223
                                                                                                                                                                                                                                                                                                                                                                                     284 STVFTRAAATLQAMATTAV--LTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTAL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217
  142 DGKQTNLRYNGGCCSETSIQVLNSSDS--TRWILTTSDSWNKANALINLLYCTPN--ACP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 SAPSTASSTTSIPTSTETTTTTPTASTTTTPTAPTTTAAPTTAATTTAVTTAASTSAETTT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ATATATSTPTTTTPTSTTTTTATTTVPTTASTTTDTTTAÄTTTÄATTTÄATTTAA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p)
Clypecies: equine herpesvirus 1
A,Note: host Equus caballus (domestic horse)
C,Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C,Accession: H56802
R,Telford, EA.R.; Watson, M.S.; McBride, K.; Davison, A.J.
R,Telford, EA.R.; March 1992
A,Description: The DNA sequence of equine herpesvirus-1.
                                                          108 LKPAKGLMSYRIITDFPSLT----RNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKP
                                                                                                                                                                                                                                                                             224 SALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 TTSSSSTSGSGQSTSSGTTNSSSSPTTSPPTTSSSPPTSTHTSSPSSTSTQSSSTAATSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 S-----MSNVESSTMNKTASWEGREASPGSSSQGSVPENQYGLPF--EKWLL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;489-797/Dōmain: equine herpesvirus 1 glycoprotein homology <EHG>F;766-790/Domain: transmembrane #status predicted <TWN>F;590/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 797;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
6.8%; Score 150.5; DB 1; Length 7
Best Local Similarity 24.3%; Pred. No. 0.025;
Matches 58; Conservative 25; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: glycoprotein; transmembrane protein
F;1-2-70-Domain: slgnal sequence #status predicted <SIG>
F;23-797/Product: glycoprotein X #status predicted <MAT>
F;23-465/Region: serine/threonine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A36805
                                                                                                                                                                                                                        257 ME---
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A;Recession: T21389

A;Accession: T21389

A;Accession: T21389

A;Accession: T21389

A;Accession: T21389

A;Accession: T21389

A;Accession: T21389

A;Accession: T21389

A;Cross-references: UNA

A;Cross-references: UNIPROT:Q09550; EMBL:Z47072; PIDN:CAA87369.1; GSPDB:GN00020; CESP:F2

C;Genetics: CSSP:F26C11.3

A;Map position: 2
                                                          A;Cross-references: UNIPROT:094317; EMBL;AL033534; PIDN:CAA22127.1; GSPDB:GN00067; SPDB:A;Experimental source: strain 972h-; cosmid c215
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 24/1; 111/1; 208/1; 272/1; 380/1; 394/3; 485/3; 586/3; 630/3; 669/3; 713/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 SSEYTPSSTESSSILDPSS--VSSAILPSSTSVEVSISSSSLSSSDPLTSSTFSSLSS-- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 SSSSSPTSTSSTISSSSSSSSSSSSTLSSSSMSS--SSSFSSSPTSSSSTISSSSSPSS 352
                                                                                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---STSSSOP---SVSSTSSSTFSSAPTSTSSSYLSSSSVVSSSSSSPSSSSSTLTSSS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 VTSQPPTTLISTVFTRA-----AATLQAMATTAVLTTTF-QAPTDSKGSLETIPFTEIS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDCVLTSSSTETGTVKFLDREFFRVFSSAEIASTTSLPTTTSPSLNCYWLSEPSNFSEWI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------NSCCSTKNI----SGDKACNLMIFDTRKTARQPNCY--LFFC-PNEEACP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F26C11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21889
                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFSLICVFCISNIFTQAFLVHQIYGNSSFTKISLNQLEGRDSQEELQRRQEIRYYGRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --GNEPVY-----TSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETGCTPTYYGYATPTSSSEPSIFSESATPSETNSYSSPVSSYSDPATSQLPSSTSFFSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 EIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASVTPSGTSOPOLATTAPPVTT
                                                                                                                                                                                                                                                                                                                                                                               9 LTYTLVII------CFLTLRLSASQNCLKKSLEDVV-IDIQSSLSK--GIR-----
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSFSSTTSSSKSSSSFSSTVSSSSTSSSTLTSSSSSSRPASSSSHS 400
                                                                                                                                                                                                                                                                             Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLTLNT-----GNVYNPTALSMSNVESSTMNKTASWEGREASPGSSS
                                                                                                                                                                                                                                                                  Query Match 7.0%; Score 154; DB 2; Length 53
Best Local Similarity 21.1%; Pred. No. 0.0087;
Matches 86; Conservative 79; Mismatches 183; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.9%; Score 151.5; Di
Best Local Similarity 22.4%; Pred. No. 0.037,
Matches 93; Conservative 46; Mismatches :
                                                                                                                              C,Genetics:
A,Gene: SPDB:SPBC215.13
A,Map position: 2
C,Superfamily: pig submaxillary mucin
                                                     A; Residues: 1-534 < LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327
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r. Biol. Chem. 267, 21375-21383, 1992
LyTitle: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr
LyReference number: A45106; MUID:93016075; PMID:1400449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Note: sequence extracted from NCBI backbone (NCBIP:116698)
; Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.M.; Clin. Invest. 88, 1005-1013, 1991
; Clin. Invest. 88, 1005-1013, 1991
; Tritle: MNC-2 human small intestinal mucin gene structure. Repeated arrays and polymorp; Reference number: A43932; MUID:91358717; PMID:1885763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Molecule type: DNA
, Residues: 1343-1350, L., 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
, Residues: 1343-1350, L., 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
, Residues: 1343-1350, L., 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>
, Residues: 1343-1350, NID:918863, PIDN:AAAS9875.1; PID:918864
, Note: sequence inconsistent with the nucleotide translation
, Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
, Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
, Holo: Lohen. 264, 6480-6487, 1989
, Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden interence number: A33532; MUID:89197956; PMID:2703501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Status: not compared with conceptual translation
'Molecule type: mRNA'
'Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
'Experimental source: bronchus
'Experimental source: bronchus
'Li, Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner,
iochem. Biophys. Res. Commun. 183, 821-828, 1992
'Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-t
'Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfamally: von Willebrand factor; von Willebrand factor type A repeat homology; von C;Superfamally: von Willebrand factor; tandem repeat
C;Keywords: g]yCoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rigum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 PENVSALPATVAVASPHTTSATPKPATL--LPTNASVTP--SGTSQPQLATTAPPVTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B. Clin. Invest. 87, 77-82, 1991, Jitle: Human bronchus and intestine express the same mucin gene. Reference number: A61257; MUID:91086481; PMID:1985113
                                                                                                                                                                                                                                             i,Molecule type: mRNA
1,Residues: 626-1895 <GU2>
1,Residues: 626-1895 <GU2>
1,Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:g186396
1,Note: sequence extracted from NCBI backbone (NCBIP:116706)
                                                                                                                                                                                                                                                                                                                                                                                                                                            'Status: not compared with conceptual translation
'Nolecule type: mRNA
'SResiduse: 2037-3020 GU3>
'GROST-references: GB:MM4132; NID:g186397; PIDN:AAA59164.1; PID:g186398
'SExperimental source: colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
;Residues: 1916-2193 -GGU4>
;Residues: 1916-2193 -GGU4>
;Residues: 1916-2193 -GGU4>
;Experimental source: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
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                                                                                                                                                                                                       A;Status: not compared with conceptual translation
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ilarity 34.1%; Pred. No. 0.15;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 2328-2342,'K',2344-2354 <XUG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:M86523
Experimental source: small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA 'Residues: 2328-2468 <XUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                     A; Accession: A45106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: B33532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A61257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: PQ0329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: PQ0328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: MUC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
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                                                                                                                                                            C4566

chitinase (EC 3.2.1.14) 2 precursor - Coccidioides immitis

chitinase (EC 3.2.1.14) 2 precursor - Coccidioides immitis

Nalternate names: chitin hydrolase homolog; CTS2 protein

c;Species: Coccidioides immitis

C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998

C;Accession: JC4566

R;Pishko, B.J; Kirkland, T.N.; Cole, G.T.

Gene 167, 173-177, 1995

A;Title: Isolation and characterization of two chitinase-encoding genes (cts1, cts2)

A;Reference number: JC4565, MUID:96144270; PMID:88566773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
A43932
mucin 2 precursor, intestinal - human (fragments)
N.Alternate names: mucin SMUC-41
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: A49963; A45106; B45106; A4332; B3552; A6157; PQ0328;
C;Species: Loning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963 AGU1>
A;Residues: L-639 AGU1>
A;Cross-references: UNIPROT:QO2817; UNIPROT:Q14884; GB:L21998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 NSCCSTKN-ISGDKACNLMIFDTRKTARQ---PNCYLFFCPNEEACPLKPAKGLMSYRII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|: | : | : | : | | : | 41 RSASTETVTTRSQEPPSTTISTWSASTETSTSSQDSPSTTISTKSAPIG----TVTTRS 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TDFPSLTRNLPSQE--LPQEDSLLHGQFSQAV-TPLAHHHTDYSKPTDISWRDTLSQ--K 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 FGSSDHL----EKLFKMD---EASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 LGGLPYADIMKEVLLRCDPDPPTSTVTSTTSASTSTQTSSQSTTMETKTLSASTTPSSPS 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVAVASPHTISATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT 288
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        A introns: 35/3; 181/2
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F;1-22/Domain: signal sequence #status predicted <SIG>F;22-39/Domain: catalytic #status predicted <CAT>F;23-860/Product: chitinase 2 #status predicted <MAT>F;63-860/Region: serine/Lhreonine-rich
F;69-860/Region: cysteine-rich
F;69-860/Region: cysteine-rich
F;90,657/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     496 QDLPSTTISTRSPETETETATTKŠQGS 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 23.9
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-860 <PIS>
A;Cross-references: GB:L41662
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JC4566
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275

Gaps

Length 3020; Indels

276 SQPPTLIS          1571 TPPFTTTPS	& 8	152 PLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDBASAQLLAYKEKGHSQSS 207 
Oy 324 ELSNLT 329 Db 1628 PPIST 1633	& 8	208 QPSSDQEIAHLLPENVSALPATYAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATT 267 510
RESULT 10 T45025 mucin MUCSB, tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Date: 21Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45025 R;Desseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A. Hidl, Chem. 272, 3168-3178, 1997	6 8 6 8	268 APPVITYTSQPPTTLISTVFTRAAATLQAMATTAVLTTTEQAPTDSKGSLETIPF 322  645 PQPTTTTSEKEVTLTTQTWTAAPPTTTVKRTTPQTVPTTTPKIPRWPLAGSGSTEQ-PW 703  323 TEISNLTLNTGNVYNPTALSMSNVESSTWNKTASWEGREASPGSSSQGSVPENQ 376  1
ous alternat	RESULT 12 \$25345 probable Nyhterna C,Species C,Date: 3 C,Aate: 3 C,Aate: 4 K,Wicessi, K,Wicessi, Yeast 8,	membrane protein YCR089w - yeast (Saccharomyces cerevisiae) ate names: hypothetical protein YCR1102 s: Saccharomyces cerevisiae 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 y. C.; Grisanti, P.; Frontali, L.
Query Match  6.8%; Score 149.5; DB 2; Length 3570;  Best Local Similarity 30.5%; Pred. No. 0.19;  Matches 62; Conservative 22; Mismatches 58; Indels 61; Gaps 10;	A;Title: A;Refere: A;Access A;Molecu A;Residu	The complete sequence of a 6146 bp fragment of Saccharomyces cerevisiae chromo connect S25345; MUID:92397594; PMID:1523889 ion: 225345 letype: DNA let
OY 204 SUSSICESDUCEANTLERNASALEATIVAAA-SENTISATEKEPTILETINASVIPSGISGE 262	A; Cross: R; Fronta submitte A; Refere A; Access A; Residu	references: UNIPROT:F22653; GB:X59720; EMBL:S43845; NID:g1907116; FIDN:CAA42254 11, L.; Grisanti, P. 11 to the Protein Sequence Database, March 1992 nce number: S19504 ion: S19504 ich: Etype: DNA s8: 1-1609 <fro></fro>
348	A, Cross- C, Genetia A, Gene: A, Cross- A, Map pour C, KeyDY F, 1592-1	A;Cross-references: EMBL:X59720; NID:g1907116; PID:e264634; PID:g1907227; MIPS:YCR089w C;Genetics: A;Gene: SGD:FIG2 A;Gene: SGD:FIG2 A;Cross-references: SGD:S0000685; MIPS:YCR089w A;Map position: 3R C;Keywords: transmembrane protein F;4-20,Domain: transmembrane #status predicted <tml> F;1592-1609/Domain: transmembrane #status predicted <tml></tml></tml>
	Query Match Best Local 3 Matches 8	/ Match Local Similarity 22.4%; Pred. No. 0.095; Local Similarity 22.4%; Local Similarity 22.4%; Pred. No. 0.095; Local Similarity 22.4%; Local Similarity 22.4%; Local Similarity 22.4%; Local Similarit
C; Accession: T34293 R; Miller, N. B; Miller, N. Bubmitted to the EMBL Data Library, April 1996 A; Description: The sequence of C. elegans cosmid F49E10. A; Reference number: Z21500	oy Oy Db	1057 IMSSSSNVISTNEKPSSTTSPYNFSSGYSLPSSSTPSGYSLSTATTINGIKTVY 1111 97 LFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHH 156 112 TTWCPLAEKSTVAASSQSSRSVDRFVSSKPSSSLSQTSIQYTLSTATTISGL 1165
	oy du	157 HTDYSKPTDISWRDTLSQKFGSSDHLE-KLFKMDEASAQLLAYKEKGHSQSSQF 209       : : :     : :     : :     1   1
A;COSB-TELETENCES: UNIFROU: QZUSYJ; EMBL: U53341; FIDN:AAC69106.1; GSFUB:GN00028; CESP:F4 A;Experimental source: strain Bristol N2; clone F49E10 C;Genetics: A;Gene: CSSP:F49E10.2 A.Man nosition: Y	o - qa	210 SSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNASV 254
Aintrons: 51/1; 92/3; 176/3; 235/3; 332/2; 514/1; 543/2; 569/3; 677/1; 732/3 Query Match 6.7%; Score 147.5; DB 2; Length 790;	ò d	255 TPSGTSQPQLATTAPPVITVTSQPPTLLSTVFTRAAATLQAMATTAVLT 304 :
	ò	

Query Match 6.6%; Best Local Similarity 21.0%; Matches 74; Conservative 47 Qy 63 CINSCCSTKNISGDKA	DD 164 CVDSFMFGSCCTHNYTDNIVLPQ  QY 119 IITDFPBLTRNLPSQELPQEDSLLHGQ  :	9 DPH 6 6	A, Cross-tereferes; CDE1131515; CATANILLES C, Keywords: glycoprotein 6.5%; Score 1 Best Local Similarity 23.9%; Pred. Natches 78; Conservative 37; Mism acches 78; Mism acches 78; Mism acches 37; Mism acches 78; Mism acches 78; Mism acches 78; Mism acches 37; Mism acches 78; Mism acches 78; Mism acches 78; Mism acches 37; Mism acches 78; Mism acches 78; Mism acches 78; Mism acches 37; Mism acches 78; Mism acches 37; Mism acches 78; Mism acches 37; Mism acches
:   : :       : :	RESULT 13 A45155 mucin FIM-C.1 - African clawed frog (fragment) C;Species: Xenopus laevis (African clawed frog) C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004 C;Date: 26-May-1994 #sequence_revision: A45155 A;Hauser, F.; Hoffmann, W. J. Biol. Chem. 267, 24620-24624, 1992 A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 A;Recession: A45155 A;Status: preliminary A;Residues: 1-662 - AHAU> A;Residues: 1-662 - AHAU> A;Residues: 1-662 - AHAU> A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PIF: 162-207/Domain: trefoil homology <trf2> F;334-394/Domain: trefoil homology <trf3> F;536-Domain: trefoil homology <trf5> F;531-S1/Domain: trefoil homology <trf5> F;621-661/Domain: trefoil homology <trf5> F;621-661/Domain: trefoil homology <trf5></trf5></trf5></trf5></trf5></trf3></trf2>	Query Match  Best Local Similarity 26.9%; Pred. No. 0.033;  Matches 49; Conservative 19; Mismatches 78; Indels 36; Gaps 5  228 ATVAVASPHTTSATPKPATLLPTATTTTTTTTTTTTTTTTTTTTTTTTTTTT	RESULT 14 A47547 A47547 A47547 Exercises Drosophila melanogaster C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: A47547 C;Accession: A47547 C;Appel, L.F. & Prout, M.; Abu-Shumays, R.; Hammonds, A.; Garbe, J.C.; Fristrom, I Proc. Natl. Acad. Sci. U.S.A. 90, 4937-4941, 1993 A;Title: The Drosophila Stubble-stubbloid gene encodes an apparent transmembrane A;Recession: A47547 A;Reterence number: A47547; MUID:93281671; PMID:7685111 A;Accession: A47547 A;Reterence number: A47547 A;Residues: 1-786 APP> A;Cross-references: UNIPROT:Q05319; GB:L11451; NID:g158511; PIDN:AAA28918.1; PID C;Genetics: A;Gene: Sb-sbd A;Cross-references: UNIPROT:Q05319; GB:L11451; NID:g158511; PIDN:AAA28918.1; PID C;Genetics: A;Gene: Sb-sbd A;Cross-references: FlyBase:PBgn0003319 C;Superfamily: serine proteinease stubble-stubbloid; trypsin homology C;Keywords: hydrolase; serine proteinase; transmembrane protein F;51-77/Domain: trynsin homology c;Keywords: hydrolase; serine proteinase; transmembrane protein F;541-7781/Domain: trynsin homology critics

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,07518; NID: 9292045; PIDN: AAB61945.1; PID: 9292046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.; Kuo, W.L.; Gum, E.; Hicks, J.W.; Gum Jr., J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ution of a unique species by expression cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144.5; DB 2; Length 505;
No. 0.035;
smatches 101; Indels 111; Gaps 15;
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                                                                                               OTAFSYTRPTKPLTLRPRPPAAPYKP----- 211
                                                                                                                                                                                                 JLLAYKEKGHSQSSQFSSDQEIAHLLPENVSAL-- 226
                                                                                                                                                                                                                       : : | : : 312
                                                                                                                                                                                                                                                              -----ATPKPATLLPTNASVTPSGTSQPQLA 265
                                                                                                                                                                                                                                                                                 ATLOAMATTAVLTTFOAPTDSKGSLETIPFTEI 325
                                                                                                                                                                                                                                                                                                                                                         : : |: :||
|SHWPSSTISITSTITITITRRITIPITT 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFSQAVTPLAHHHTD-----YSKPTDISW 168
                                                                                                                                                        8-Nov-1994 #text_change 09-Jul-2004
146; DB 1; Length 786;
No. 0.048;
smatches 162; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kbone (NCBIN:128397, NCBIP:128399)
                                                                                                                                                                                                                                                                                                                                                                                                TMNKTASWEGREASPGSSSOGSVPENQ 376
                                                                                                                                                                                                                                                                                                                                                                                                                       in (fragment)
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OY 288 TRAMATLQAMATTAVLTTTEQAPTDSKGSLEF-IPFTEISNLTLNTGNVYNPTALSMSNV 346
:::| || || || || ||
Db 302 SPLSSTGPMTATSIKTTTYPTPSHPQTTLTTHVPPFSTSSVTPSTHTVITPTHAQMST- 360
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מייים בספספס נת מסתיים נשמים השים בי בי	34 / ESSIMNIASWEGREASPGSSSQGSVP	

*장* 원

Search completed: April 26, 2005, 21:52:31 Job time : 55 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 26, 2005, 20:26:45; Search time 122 Seconds (without alignments) 1809.067 Million cell updates/sec Run on:

Title: Perfect score:

US-10-735-014-83
2211
1 MFFGGEGSLTYTLVIICFLT......LRRKRYSRLDYLINGIYVDI 431 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		Description	Q9h8j5 homo sapien	Q95kg7 macaca fasc	Q9nw60 homo sapien	Q9cr33 mus musculu	Q8k0i0 mus musculu	Q8vcp2 mus musculu	Q9h2k4 homo sapien	Q9d8n1 mus musculu	Q96f05 homo sapien	Q8wwq4 homo sapien	Q7ytr7 caenorhabdi	homo	homo	homo	homo	homo	Q17921 caenorhabdi	Q6ci85 yarrowia li	094317 schizosacch	Q09550 caenorhabdi	Q9xzz8 litomosoide		-	P54197 coccidioide	Q02817 homo sapien		Q8tfg9 schizosacch	Q66vc3 equid herpe	P98088 homo sapien	_	Q6a564 bacteroides
SUMMARIES		ID	MNS1_HUMAN	MNS1_MACFA	Q9NW60	MNS1 MOUSE	OBKOIO	Q8VCP2	Q9H2K4	Q9D8N1	Q96F05	Q8WWQ4	Q7YTR7	Q685J2	0685J3	.014887	Q8WWQ5	000446	017921	Q6CI85	094317	YQU3_CAEEL	09XZZ8	VGLX_EHV1B	Q6DLE0	CHI2_COCIM	MUC2_HUMAN	MUSB HUMAN	YL61_SCHPO	Q66V <u>C</u> 3	MUSA_HUMAN	Q6V4A2	Q6A564
		g :	Н	7	~	-	~	7	~	7	~	~	~	7	7	7	~	7	7	~	7	Н	7	Н	N	н	-	-	-	~	-	~	0
		Match Length DB	431	431	397	414	194	392	449	392	449	1349	519	4262	4493	477	2448	328	169	784	534	1240	382	797	797	. 860	5179	5703	943	791	1233	513	2299
•	Query	Match	100.0	92.2	91.5	52.7	22.7	8.9	8.9	8.9	8.5	8.7	7.6	7.4	7.4	7.3	7.1	7.1	7.0	7.0	7.0	6.9	6.8	6.8	6.8	6.8	6.8	6.8	6.7	6.7	6.7	6.7	6.7
		Score	2211	2039	2022	1164.5	503	197.5	197	196.5	188	180.5	168	163	163	160.5	157.5	156.5	155.5	154.5	154	151.5	150.5	150.5	150.5	150.5	149.5	149.5	149	148.5	148.5	148	148
	Result	No.	7	8	e	4	S	φ	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q20599 caenorhabdi Q95qf5 caenorhabdi P25653 accotaromyc Q05049 xenopus lae Q8V0m4 equid herpe Q86ak1 dictyosteli Q6bgg debaryomyce Q05319 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q24017 drosophila Q102w3 human herpe Q90487 caenorhabdi Q8tax7 homo sapien
Q20599 Q95QF5 PIGZ_XEMIA MUCI_XEMIA Q8V0M4 Q6BGAKI Q6BGAKI Q240I7 Q9NYE4 Q702W3 Q9NYE4
попринопопи
790 1609 662 316 472 786 629 786 629 716 .901
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147.5 147.5 147.5 147.5 146 146 146.1 145.5 145.5 145.5 145.5
6 6 6 6 6 7 7 8 8 8 9 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K.; Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley, C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., ន្ទន្ទន

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MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-223825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wann J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakebley R.W., Touchman J.W., Scheutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Warra M.A.,
Butterfield W.B., Ooder W.B., Warra M.A.,
Butterfield W.B., Wooder W.B., Warra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                              ø
                                                                                                                                           "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; denome Res. 13:2265-2270(2003).
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Yi S., Yu G., Yuana J., Wieand D., Woods K., Xie M.-H., Yansura D.
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANSC.

Thr-rich.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
V -> I (in Ref. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-i. SUBCELLUTAR LOCATION: Type I membrane protein (Potential).
-i. SIMILARITY: Contains 1 MANSC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 431;
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MANSC domain containing p
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189136416F0F89AE CRC64;
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SIGNAL 1 26
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EMBL; AY358563; AAQ88926.1; -.
EMBL; BC032998; AAH32998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR011106; MANSC_N.
Pfam; PP07502; MANSC; 1.
PROSITE; PS50986; MANSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46810 MW;
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409
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431 AA;
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DOMAIN
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DOMAIN
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                             420
                                                                                                                                                                                                                                                                                                                                                                                                            420
                                                                                                                                                                                240
                                                                                                                                                                                                     HIEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQETAHLLPENVSALPATVAVASPHTTSA 240
                                                                                                                                                                                                                                                                 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                                                                     EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
                                                                                                                                               TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
                                                                                                                                                                                                                                               TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
                                                                                                                                                                                                                                                                                                             AVLITIFQAPIDSKGSLETIPFIEISNLTLNTGNVYNPTALSMSNVESSTWNKTASWEGR 360
                                                                                                                                                                                                                                                                                                                                             360
EASPGSSSQGSVPENQYGLPFEKWLIGSLLFGVLFLVIGLVILGRILSESLRRKRYSFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Υ.
                                                                                                                  TDFPSLTRNLPSOELPOEDSLLHGOFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD
                                                                                                                                                                                                                                                                                                                                 AVLTTTEQAPIDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTWIKTASWEGR
                                                                                                                                                                                                                                                                                                                                                                                              HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
MANSC domain containing protein 1.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2001) to the EWBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 MANSC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
MANSC domain containing protein 1 precursor (QtrA-13483).
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InterPro; IPR011106; MANSC_N.
Pfam; PF07502; MANSC; 1.
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SIGNAL
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Pubmed=14702039; DOI=10.1038/ng1285;

Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Awakamatsu A., Hayashi K., Satc H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sammetc J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Yamametc J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 12, Last annotation update)
Hypothetical protein FL10298.
Hypothetical protein FL10298.
Buken sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                         (Potential). (Potential).
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Linked (GlcNAc. ..) (Potential)
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BF10996E87F76G69 CRC64;
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Pred. No. 5.5e-125;
9; Mismatches 24; Indels (
Potential.
Cytoplasmic (Potential).
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Best Local Similarity 92.3
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Ranchori K., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
Ranchori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
Taylya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
Musashino K., Yuuki H., Oshima A., Sasaki N., Imose N.,
Wasashino K., Yuuki H., Oshima A., Sasaki N., Sano S.,
Noriya S., Momiyama H., Ichihara T., Shiohata N., Sano S.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fujkuzumi Y.,
Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
A. Nakabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
Ond T., Xamakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
A. Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Makai K., Yada T., Nakamura N., Ohara O., Isogai T., Sugano S.,
Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Makai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
Makai M., Matanabu A., Nakamura Y., Ohara O., Isogai T., Sugano S.,
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Makai M., Matanabu A., Ohara O., Isogai T., Sugano S.,
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Pred. No. 6.4e-124;
0; Mismatches 0;
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EMBL, AKO01160; BAA91526.1;
InterPro; IPR011106; MANSC.N.
Pfam; PP07502; MANSC.1.
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Best Local Similarity 92.1%;
Matches 397; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=C57BL/6J; TISSUE=Cecum, Colon, and Medulla oblongata;

MEDLINE=25394681; PubMed=1246681; DOT=10.10.38/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Baito R., Suzuki H., Yamanaka I., Kiyosawa H.,

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Baldarelli R., Gariboldi M., Glasi C., Godzik A., Gough J.,

Anala E., Dragami T.A., Fletcher C.F., Forrest A., Srazer K.S.,

Gasterland T., Gariboldi M., Glasi C., Godzik A., Gough J.,

Romadaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

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Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Angashima T., Nunata K., Pontius J.U., Qi D., Ramachandran S.,

Retrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S.,

Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sandelin A., Schneider C., Semple C., Wang Y., Watanabe Y., Wells C.,

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Analyazaki A., Sakai K., Sasaki J., Aizawa K., Arakawa T., Flukuda S.,

Ayaraki A., Hashizume W., Imotani R., Inder B.S., Rogers J.,

Nasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,

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Nasunishi A., Yashikawa I., Akawa I., Akawa K.,

Shiraki T., Waki K., Sasaki D., Sibata K., Shinagawa I.,

Nasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,

Nasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J.,

Nasunishi A., Rogers J., All A., A., All A., A., All A., A., A.,
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MELSCHOL S. P. Feringold E. A., Grouse L., Bhat N. K.,

MELSCHOL S. P., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N. K.,

METCHOL S. M., Morden H., Moore T., Max S.I., Wanja J., Haich F.,

MENAS S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MENAS S.A., McEwan P.J., McKernan K.J., Malek J.A., Guartane P.H.,

MILLION D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,

Rabes S.A., McAdan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milting M., Schein J.E., Jones S.J.M., Marra M.A.,

Meneratical Y.S.M., Krzywinski M.I., Skalska U., Smallus D.E.,

Meneratical A., Schein J.E., Jones S.J.M., Marra M.A.,

Meneratical A., Schein J.E., Jones S.J.M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Schein J.E., Jones S.J.M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

Meneratical A., Marken M. M., Marra M.A.,

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Meneratical A., Marken M., Marra M.A.,

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Contains 1 MANSC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
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                                                           WCBI_TaxID=10090;
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EMBL; AK018660; BAB31329.1; -. EMBL; AK018635; BAB31319.1; -.

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301 AVLTTTROAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTWNKTASWEGR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 EASPGSSSQGSVPENQYGLPFEKWLLIGSILFGVLFLVIGLVLLGRILSESLRRKRYSRL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 RVSVGSASLNKGPKSQHGLSFEKWLLIGTLLCGVLFLVIGLVLLGRMLVEALRRKRYSRL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRII 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSD 180
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52.7%; Score 1164.5; DB 1; Length 414;
Best Local Similarity 59.9%; Pred. No. 6.1e-68;
Matches 258; Conservative 37; Mismatches 119; Indels 17;
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Extracellular (Potential)
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Cytoplasmic (Potential).
MANSC.
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Last annotation update)
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I -> V (in Ref. 2).
R -> G (in Ref. 2).
R -> G (in Ref. 2).
M -> T (in Ref. 2).
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         EMBL; AK033557; BAC28357.1; -...
EMBL; AK046837; BAC32892.1; -...
EMBL; BC039930; AAH39930.1; -...
MGD; MGI:1914979; 9130403P13Rik.
InterPro; IPR011106; MANSC N.
Pfam; PF07502; MANSC; 1.
                                                                                                                                                                                                                                                                                                                                                                            44822 MW;
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01-0CT-2002 (TEMBLrel. 22,
01-0CT-2002 (TEMBLrel. 22,
01-MAR-2004 (TEMBLREl. 26,
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TRANSMEM
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus
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01-MAR-2001
01-MAR-2004
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                                                                                                                                                                                                                                                                                                                                               210
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                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                         227 PATVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTV
                                                                                                                                                                                                                                                                                                                                                                                            FT-----BVVTHQAALTNTFQAHTDSKGILETMPFQGGSTLT-----SDPRHGKSSTS
                                                                                                                                                                                                                                                                                                                                                                                                          347 ESSTMNKTASWEGREASPGSSSQGSVPENQYGLPFEKWLLIGSLLFGVLFLVIGLVLLGR
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                Length 194;
                                                                                                                                                                                                                                                                                                                               56; Indels
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
STRAIN=FVB/N; TISSUE=Liver;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031372; AAH31372.1; -.
MGD; MG1:1914979; Manecl.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
                                                                                                                                                                                                                                                                                                  194 AA; 20701 MW; 11C1F299E1FB3C44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                22.7%; Score 503; DB 2; 59.5%; Pred. No. 3.5e-25;
                                                                                                                                                                                                                                                                                                                               Matches 122; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                        sequences."
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01-OCT-2002 (TrEMBLrel.
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01-MAR-2002 (TrEMBLrel.
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Name=1810055G02Rik;
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                                                                                                                                                                                                                                                                                                                        Local Similarity
                             NCBI_TaxID=10090;
                                                                                                                                                                                                        and mouse cDNA
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STAIN=FVBB/N; TISSUB=Liver;

STAIN=FVBB/N; TISSUB=Liver;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A traubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A traubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A traubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A traubberg R.P., Jozdan H., Moore T., Max S.I., Wang J., Haish F.,

A papleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raba S., Worley K.C., Hale S., Garcinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

A Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%; Score 197.5; DB 2; Length 392; 26.5%; Pred. No. 7.3e-05;
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
SEQUENCE 392 AA; 41081 MW; 1D79796C791211FA CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Mismatches 115;
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(TrEMBLrel. 16, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences."
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us-10-735-014-83.rup

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SEQUENCE
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---LPINASV--TPS--GISQPQLAITAPPVITVISQPPTILISTVFTRAAATLQAMAIT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 MEVITEDI------SRIDVSEP-----ATSGGAADGVISIAPIAVAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHT----TSATPKPATL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 STTAA-----SITTAASSMTVASSAP-TTAASSTTVASIAPTTAASSMTAASSTPMTL 164
                                                                                                                                                                                                                                                                                                                                     13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN 72
                                                                                                                                                                                                                                                                                                                                                    76 TUTING-----TSAAHLNS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus 10 day old male pancreas CDNA, RIKEN full-length enriched
                                                                                  SEQUENCE FROM N.A. MEDLING 1401438; DOI=10.1006/geno.2000.6492; MEDLINE=21295044; PubMed=11401438; DOI=10.1006/geno.2000.6492; Twells R.C.J., Metzker M.L., Brown S.D., Cox R., Garey C., Hammond H., Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.; "The sequence and gene characterization of a 400-kb candidate region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 ALPAPTSTSTGRTPSTTATGHPSLSTALAQVPKSSALPRTATLATLATRA----QTVATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPEPAPTPTV--VTTTKAQAREPTASPVPVPHTSPIPEMEAMSPTTQPSPMPYTQRAAGP
                                                                                                                                                                              SEQUENCE FROM N.A.

Twells R.C., Merzker M.L., Brown S.D., Cox R., Garey C., Hammond H., Hey P.J., Levy E., Nakagawa Y., Philips M.S., Todd J.A., Hess J.F.; Submitted (MAY-200) to the EMBL/GenBank/DDBJ databases.

EMBL, AF264781, AAG36936.1,
                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               196;
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                                                                                                                                                                                                                                                                                                             166; Indels
                                                                                                                                                                                                                                         InterPro; IPR001395; Aldo/ket red.
PROSITE; PS00063; ALDOKETO REDUCTASE 3; UNKNOWN 1.
SEQUENCE 449 AA; 46100 MW; 11C8B0FCC3BBF921 CRC64;
                                                                                                                                                                                                                                                                                       8.9%; Score 197; DB 2;
22.2%; Pred. No. 9.3e-05;
ive 49; Mismatches 166
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                                                                                                                                             for IDDM4 on chromosome 11q13.";
Genomics 72:231-242(2001).
                                                                                                                                                                                                                                                                                                   22.28;
                                                                                                                                                                                                                                                                                                   Best Local Similarity 22.2
Matches 117; Conservative
   JM4E3.
Name=Cllorf24;
---ions (Human)
                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                             NCBI_TaxID=9606;
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STRAIN-CSTBL/63; TISSUB-Pancreas;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiranco K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Rurihara C.,
Matsuyama T., Miyazaki A., Nishii K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Maramatsu M., Hayashizaki Y.,
Maramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

REMBL, MGD: 181005502Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOI=10.1016/S0076-6879(99)03004-9;
library, clone:1810055G02 product:hypothetical Threonine-rich region containing protein, full insert sequence.
Name=1810055G02Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-673 (2002)
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                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/60; TISSUE-Pancreas;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CSTBL/65; TISSUB=Pancreas;
MEDLINE=99279253; PubMed=10349636; DOI=10.101
Carninci P., Hayashizaki Y.
Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in Hayashizaki Y., in 
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UENCE 392 AA; 41095 MW; 6BBA958C73489
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The FANTOM Consortium,
the RIKEN Genome Exploration Resea
                                                                                                                                                                                                                         Mus musculus (Mouse)
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GO; GO:001602
Hypothetical
SEQUENCE 39
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                        Huang Y.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Richanner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
And S.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Brownstein M.J. Usdin K., Farmer A.A., Rubin G.M., Hong L.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Mark G. G., Gunarathe P. H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Raywinski M.I., Skalska U., Smallus D.E., Bickson M.C.,
Raywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
A. Jones S.J., Marra M.A.,
                                                                                                                                                              129
                                                                                                                                                                                                                                                                                                       ----VTSQPPTTLISTVFTRAAA 292
                                                                                                                                                                                                                                                                                                                                                     248
                                                                                                                                                                                                                                                                                                                                                                                                 TLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTMN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 KTASWEGREASPGSSSQGSV------PENQYGLPFE-----KWLLIGSLLFG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GTAS-----AGPTSRSSGDIKVPTTDSCQPSTQGQYLVTIDALTPSLVNKMLLLVVLLVG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                    216 AHL------LPE-NVSALPAT--VAVASPHTT------SATPKPATLLPT
                                                                                                                                                                                                                                       249 TVPARATSLSPDVDVISPTTQPS--PTLP----TQGTGG--PGTLLTTEQVGTKTTS
                                                                                                           156 HHTDYSKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEI
                                                                                                                                                            -----TREGITDRV-----TSRILAVPISSGPSSAEQIRPITI
                                                                 Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                               97;
                     Length 392;
                                                                 Indels
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Last annotation update)
frame 24 (FP2568) (Cllorf24).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
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       8.9%; Scote _ 26.1%; Pred; No. 8.4e-v., ..., ..., ..., ..., ..., ..., Mismatches 110; ...msasAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 VLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD
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                                                               88; Conservative
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                                                                                                                                                         88 HGTNTSTPT
                                           Similarity
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                 Query Match
Best Local
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                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 ANTSSPMSTRPSPSKHMPSDTAASPVPPMRPQAQGPISQVSVDQPVVNTTNKSTPMPSNT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SMS-NVESSTMNKTASWEG- 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFPSLTRNLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQEDCINSCCSTKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                   Oin W.X., Zhao X.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWLLIGSLIFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVD 430
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                                                                                                    to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00063; ALDOKETO REDUCTASE 3; UNKNOWN 1.
SEQUENCE 449 AA, 46142 WW; BF984AA360F6C415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 188; DB 2; 22.0%; Pred. No. 0.00036;
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FROM N.A.
Zhou X.M., Zhang P.P., Jiang
Gu J.K.,
(APR-2001) to the EMBL/GenBan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; BC011765; AAH11765.1; -.
EMBL; AF370372; AAQ15208.1; -.
EMBL; AY358754; AAQ89114.1; -.
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                                                                                                                                           [4]
SEQUENCE FROM N.A.
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Q8WWQ4;
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nterPro; IPR006209; EGF like.
InterPro; IPR011047; Quin alc_DH_like.
InterPro; IPR000082; SEA.
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                                                                                                                                    EMBL; Z81044; CAE17706.1; -.
WormBase; WBGene00007828; C30H6.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS50024; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Pancreatic adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pancreatic adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                          WormPep; C30H6.11; CE34720.
 investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted mucin MUC17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 58; Conserv
                                                         SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEOUENCE FROM N.A.
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                                                                                               Mortimore B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moniaux N.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-0CT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=MUC17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
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                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 GGDKE-TÝNNIIRSGEKIČRRPQEITRLÓ-CRAKSHPEVSIEHLGQVVQCSREEGL---- 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 GLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQ------AVTPLAHHHTDY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          607 VIAPSPLVGEPPAQTQSTSSWQKSRTTTLVTSSITSTTQTSTTSAPITSTTPASIPSTTS 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 SKPTDISWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 ENVSALPATVAVASP--HTTSATPKPATLLPTNASVTP------SGTSQPQLATTA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STISA-PITSTISAPITSTISAPIASTITSAPISSAPITSTSAPITSTAPITSTISAPITSTIS 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 PPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 PVYTSTQEDCINSCCSTKNISGD-KACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770 APTISTTSTPQTSTISSPTTSTTPTPQTSTTSSPTTSTTSAPTTSTTSAPTTSTPQT 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 GGEGSLIYTLVI----ICFLTLRLSASQNCLKKSLEDVVID-----IQSSLSKGIRGNE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APTTSTTSAPTTS------TTSAPTTSTTSTTSTTSSAPTSSTTSAPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                            MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763; Escande F., Aubert J.P., Porchet N., Buisine M.P.; "Human mucin gene MUC5AC: organization of its 5'-region and central
                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

8.2%; Score 180.5; DB 2; Length 1349;
Best Local Similarity 21.6%; Pred. No. 0.0044;
Matches 88; Conservative 62; Mismatches 174; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 TLNTGNVYNPT-ALSMSNVESSTMNKTASWEGREASPGSSSQGSVPE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::: | | : | | : | : | : | : | 310 SITSAPITSTISAPITSTIPQ 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                  1349 AA; 135599 MW; 4DC3C1544F1E5EBA CRC64;
 Created)
Last sequence update)
Last annotation update)
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1-MR-2004 (TrEMBLrel 26, Last annotation update)
Hypothetical protein C30H6.11.
ORFNames=C30H6.11;
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                                                                                                                                                                                                                                                                                       358:763-772 (2001)
01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                           Biochem. J. 358:763-772(2001
EMBL; AJ298318; CAC83675.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                  1349
                                                                                               Homo sapiens (Human)
                                                         Mucin 5 (Fragment).
                                                                                                                                                                                                                                                                           repetitive region."
                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                             Name=MUC5AC;
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SEQUENCE
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270 AYNYYNYTNDNAHYD-----NNSNNHNYSENFWRLMLSLPIAFSINFTLLNSIYLQHMK 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 TVAVASPHTTSATPKPATLLPTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----STMNKTASWEGREASPGSSSQGSVPEN----QYGLPFE---KWLLIGSL----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                             38;
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                                                                                                                                                                                                                                                                                                                              Length 519;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                       GO; GO: 005529; F: sugar binding; IEA.
InterPro; IPR01304; Lectin_C.
SMART; SM00034; CLECT; 1.
Hypothetial protein.
SEQUENCE 519 AA; 56012 MW; 93C2CFF9EC339D1A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                    7.6%; Score 168; DB 2;
27.1%; Pred. No. 0.0087;
cive 22; Mismatches 96,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 YDLTSILFNALGTVTL-----LMRKIFCNIQY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 163; DB 2; 22.7%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- LFGVLFLVIGLVLLGRILSESLRRKRYSRLDY 422
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348

288 214 127

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SMPASTWKVASSEAITLLTTPVEISTPVTISAQASSSPTTAEGPSLSNSAPSGGSTPLTR 279
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                                                                                                                                                                                                                 DHLEKL-----FKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAV 232
                                                                                                                                                                                                                                                                                                                                                                                                         QPPTTLI-----STVFTRAAATLQAMATTAVLTTTFQAPTDSKG-SLETIPFTEISNLT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 MPLSVMLVVSSEASTLSTTPAATNIPVITS---TEASSSPTTAEGTSIPTSTYTEGSTPL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EASAQLLAY----KEKG----HSQSSQFSS--DQEIAHLLPENVSALPATVAVAS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 SHPEVSIEHLGQVVQCSREEGLVCRNQDQQPFYMCLNYEVRVLCCETPKGCPVT---ST 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHTTSATPKPATLLPTNAS-----VTPSGTSQPQLATTAPPVTTVTSQPPTTLI 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVTAPSTPSGRATSPTQSTSSWQKSRTTTLVTTSTTSTPQTSTTSAPTTSTTSAPTTSTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STVFTRAAATLQAMATTAVLTTTFQAPTDSKGSLET---IPFTEISNLTLNTGNVYNPTA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : | : | : | : | SAPTISTISARTISIISAPTISTISART 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 LNTGNVYNPTA-----LSMSNVESSTMNKTA-----SWEGREASPGSSSQGSVP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMTPTESRITISESTSDSTTLFPSPTEDTSSPTTPEGTDVPMSTPSEESISSTMA--FVST
                                                                        SQHVRTGSATNTATGTTSTNVVEPRMYL----SCSTNPEMTSIESSVTSDTPGVSST
                                                                                                                       RNLPSQELPQEDS-----LLHGQFSQAVTPLAHHHTD--YSKPTDISWRDTLSQKFGSS
                                                                                                                                                                                                                                                                                                             ASPHTTS--ATPKPATLLPT-------NASVTPSGTSQPQLATTAPP--VTTVTS
                             TKNISGDKACNLMIPDTRKTARQPNCYLPPCPNEEACPLKPAKGLMSYRIITDFP--SLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucuo saptaens (numan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Tracheobronchial mucosa; Guyonnet-Duperate V., Audie J., Debailleul V., Laine A., Buisine Guyonnet-Duperate V., Audie J., Debailleul V., Laine A., Buisine Coultina Galiegue S., Pigny P., Aubert J., Porchet N.; "Characterization of the human mucin gene MUC5AC: a consensus cysteinte-rich domain for 11p15 mucin genes."; Biochem. J. 0:0-0(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 24.4%; Score 160.5; DB 2; Length Similarity 24.4%; Pred. No. 0.024; Conservative 42; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 AA; 50666 MW; E7360031B4A51311 CRC64;
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Last annotation update)
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NON TER 1
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01-NOV-1996 (
01-JUN-2003 (
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                                                                                                                                                                  109
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SEQUENCE
                                                                        26
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                                                                                                                                                                     56 SQHVRIGSAINTAIGITSINVVEPRMYL----SCSINPEMISIESSVISDIPGVSST 108
                                                                                                                                                                                                                                                                 | :|:| | : :|: | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1.0 | 1
                                                                                                                                     70 TKNISGDKACNIMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP--SLT 127
                                                                                                                                                                                                                                  128 RNLPSQELPQEDS-----LLHGQFSQAVTPLAHHHTD--YSKPTDISWRDTLSQKFGSS 179
                                                                                                                                                                                                                                                                                                                              180 DHLEKL-----FKMDEASAQLIAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAV 232
                                                                                                                                                                                                                                                                                                                                                                                                                          233 ASPHTTS--ATPKPATLLPT------NASVTPSGTSQPQLATTAPP--VTTVTS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPPTTLI-----STVFTRAAATLQAMATTAVLTTTFQAPTDSKG-SLETIPFTEISNLT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 MPLSVMLVVSSEASTLSTTPAATNIPVITS---TEASSSPITAEGTSIPTSTYTEGSTPL 336
                                                                           69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 ISTPASTMPVATSEMSTLSITPVDTSTLVTTSTEPSSLPTTAEATSMLTSTLSEGSTP 394
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LCLTILVLS-------LLPPQAAARQGLSVNRAVWDGGGCISQGDVLNRQCQQL
                                                16 ICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTS----TQEDCINSCCS--
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       Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4493 AA; 451718 MW; 06B1D6C680499AAS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moniaux N.B.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL606307; CAES4435.1;
InterPro; IRR008985; Cona like_lec_gl.
InterPro; IRR006209; EGF like.
InterPro; IRR011047; Quin_alc_DH_like.
InterPro; IRR000082; SEA.
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Last annotation update)
  Mismatches 161;
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PROSITE; PS50024; SEA; 1.
  70;
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(TrEMBLrel. 28, I
Conservative
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Local 95; Conserva
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9 LCLLTLVLS-
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Q685J3;
Matches
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2077 TFTTHMPSASTEQPIATSRGGPTATSVTQGTHTTPVTRNCHPRCTWTTWFDVDFPSPGPH 2136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2193 RNQDQQGPFKMCLNIEVRVLCCETPKGCPVT---STPVTAPSTPSGRAISPTQSTSSWQK 2249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2310 PVPTTSTTSAATTSTISAPTTSTTS---VPGTTPSPV-LTTSTTSAPT-----TR 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2034 CYNYEIRIQCCETVNV------CRDITRPPKTVATTRPTPH-----PTGAQTQT 2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2250 SRITILVITISTISTPQTSITYAHTTSTTSAPTARTTSAPTISTISVPITSTISGPKTIPS 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CIN----SCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 RIITDFPSLTRNLP---SQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISW----- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 ---RDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSS-----QFSSDQ----313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ATLQAMATTAVLTTTFQAPTDSKGSLETIPFTEISNLTLNTGNVYNPTALSMSNVESSTM 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 ------EIAHLLPENVSALPATVAVASPHTTSATPKPATLLPTNAS---- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 -----VTPSGTSQPQLATT-----AP-----PVTTVTSQPPTTLISTVFTRAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE_Trachea;
MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;
MEDLINE=21426417; PubMed=11535137; DOI=10.1042/0264-6021:3580763;
BECAUGE F., Aubert J.P., Porchet N., Buisine M.P.;
"Human mucin gene MCC5AC: organization of its 5'-region and central repetitive region.";
repetitive region.";
sinchem. J. 3381763-772(2001).
EMBL; AJ298317; CAC83674.1; -..
HSSP; P56682; ICCV.
                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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7.1%; Score 157.5; DB 2; Length 2448;
Best Local Similarity 23.1%; Pred. No. 0.29;
Matches 87; Conservative 38; Mismatches 142; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2448 AA; 260968 MW; A5C1BD627844D952 CRC64;
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Last annotation update)
                        252 TSTISAPISSTISTPQISKISAAISSTISGS 282
341 LSMSNVESSTMNKTASWEGREASPGSSSQGS 371
                                                                                                                                              PRT; 2448 AA.
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NON_TER 2448 2448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:7515; MUC5AC.
Pfam; PF01826; TIL; 2.
Pfam; PF00094; VWD; 3.
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  Mucin 5 (Fragment)
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SEQUENCE
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                   RESULT 1
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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-MODEL=frame+ p2n. model - DEV=xlp
-MODEL=frame+ p2n. model - DEV=xlp
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-Gegnz_1/USFTO_spool_p/US10735014/runat_26042005_113100_7413/app_query.fasta_1.583
-DB-GenEmbl - OFWT=fastap - SUPFIX=rge -MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=buman40 . cdi - LIST=45
-UOTALIGN=200 - THR_SCORE=pct - THR MAX=100 - TRANS=buman40 . cdi - LIST=45
-OOTALIGN=200 - THR_SCORE=pct - THR MAX=100 - MAXIEN=200000000
-USER=US10735014 @CGN 1 1 5600 @runat_26042005 113100_7413 - NCPU=6 - ICPU=3
-NO_WMAP - LARREQUERY - NEG SCORES=0 - WAIT - DSPBELOK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPDP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - FGAPOP=6
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AR429104 Sequence
AR534995 Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                              nucleic search, using frame_plus_p2n model
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               GAAAATGTGAGTGGGCTCCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT
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Mismatches: 0
Indels: 0
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1 (bases 1 to 2284)

Winterbottom, J.M., Shimp, L., Boyce, T.M. an Implant, method of making same and use of treatment of bone defects

Patent: US 6478825-A 514 12-NOV-2002;

Location/Qualifiers
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Sequence 514 from patent US 6478825.
AR252736 GI:27300644
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/organism="unknown"
/mol_type="genomic DNA"
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PI WILLIAM I WOOD, AUDREY GODDARD, AUSTIN L GURNEY, JEAN YUAN, KEVIN PI P BAKER,
PI JIAN ZHENG
PC CI2N15/09, C07KL4/47, C07KL6/18, C12N1/19, C12N1/21, C12N5/10, PC C12P21/08, C12P21/08, C12N15/00, C12N5/00
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/organism='Homo sapiens (human)'.
Location/Qualifiers
1. .2284
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/organism="Homo sapiens"
/db_xref="fexon:9606"
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Polypeptides and nucleic acids encoding
Location/Qualifiers
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1 (bases 1 to 2284)
Filvaroff,E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gu and Wood,W.I.
and Wood,W.I.
Artibodies against a secreted polypeptide that stimulates of proteoglycans from cartilage
Patent: US 6734288-A 82 11-MAY-2004;
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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    /organism="unknown"
    /mol_type="genomic DNA"

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 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr
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US-10-735-014-83 (1-431) x AX403627 (1-2284)  QY	41 IleGlnSerSerLeuSerLygGly1leArgGlyAsnGluProValTyrThrSerThrGln 60	Db 406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAAGCATGTAAC 465  Qy 81 LeumetllePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  Qy 81 LeumetllePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100  Db 466 TTGATGATCTTCGACACTGGAAAACAGCTAACAACTGCTACTATTTTTTTT	Db 526 CCCAACGAGGAACCTGTCCATTGAAACCAAGGACTTATAGAGTTACAGGATAATT 585  Qy 121 ThraspPheroSerLeuThratagasnLeuProSerGlnGluLeuProGlnGluAspSer 140  Db 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGAGTTACCCCAGGAAGATTCT 645	141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 16 [	DD 706 TCAAAGCCCACCGATATCTCATGGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765  QY 181 HisLeuGluiyeLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200  QY 16	Db   826   AAGGCCATTCTCAGAGTTCTCTTTTCTCTGATCAGAATTGCTCATCTGCTGCTTT   885	Qy 241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260	Qy 261 GlnProGlnLewAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280	Oy 281 ThrLeuIleSerThrValPheThrArgAlaAlaThrLeuGlnAlaMetAlaThrThr 300	Qy         301 AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320           Db         1126 GCAGTTCTGACTACCACCTTTCAGGCACCTACGAAAGGCAGCTTAGAAACCATA 1185	Oy 321 ProPheThrGlulleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340	Qy 341 LeuSerMetSerasnValGluSerSerThrMetAsnLysThralaSerTrpGluGlyArg 360
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I (clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chon, J., Chow, B., Chul, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, O., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Fifort to Identify Novel Human Secreted and Transmembrane Proteins:
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Homo sapiens clone DNA45410 FFGG316 (UNQ316) mRNA, complete cds.
AY358563
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Submitted (01-MG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA WAY, South San Francisco, CA 94080, USA
Location/Qualifiers
             GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro
                                                                               PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly
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Genome Res. 13 (10), 2265-2270 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr
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                                                                                                                                                                                                                                   41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln
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Qy         361 GluhlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380           Db         1339 GAGGCCAGTCCAGGCAGTTCTCCCCAGGGATGTTCCAGAAATCAGTACGCCTTCCA 1398           Qy         381 PheGluLyBTrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVall116Gly           Db         1399 TTTGAAAATGGCTTCTTATCGGGTCCTTTTGGTTCCTGGTTCCTGGTATAGGC 1458           Qy         401 LeuValLeuLeuGlyAsgTleLeuBerGTGTCTTTTGGTGATCCTCTGGTATAGGC 1458           Db         1459 CTCGTCCTCTGGGTAGAATCCTCTCGGAATCACTCCGCAGGGAAACGTTACTCAAGACTG 1518           Qy         421 AspTyrLeuIleAsnGlyIleTyValaspIle 431           Db         1519 GATTATTTGATCAATGGGATCATTAGTGGACATC 1551	7-DEC- mamoto T. mamoto T. EDVVID EDVVID ENCYLF FSSDOE TAPPVT TAPPVT TAGACA TAGACA TAGACA TTGACA TTGACA TTGACA	Qy 41 IleGlnSerSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln 60 

LOCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 ATGTTCTTCGGGGGGGGAGAGGGGGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA
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     Location/Qualifiers
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                                                                                                                                                                                         PRI 30-JAN-2004
                                                                                                                                                                                                                                                         AKO23622.1 GI:10435603
Oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute
                                                                                                                                                                                   AK023622 2297 bp mRNA linear
Homo sapiens cDNA FLJ13560 fis, clone PLACE1007877.
                                                     421 AspTyrLeulleAsnGlylleTyrValAspile 431
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Direct Submission
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SKPTDI SWRDTLSQKFGSSDHLEKLFKMDEASAQLLAYKEKGHSQSSQFSSDQEIAHL
LPENVSALPATVAVASPHTTSATPKRATLLPTNASYTPSGTSQPQLATTAPPVTTVTS
OPPTILISTVYPTRAAATLQAMATTAVLTTFQAPTDSKGSLETI PFTEI SNLTLNTGN
VYNPTALSNGNVESSTENKTRANGGREASPGSSSQGSVPENQYGLPFEKWLLIGSLLF
GVLFLVIGLVLGRILSESLRRKRYSRLDYLINGIYVDI"
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| Ma xref="GG1:21542503"
| Ab xref="Locus1b:54682"
| Aranslation="MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSKGIRGNEPIYTSTQEDCINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPN
EEACPLKPAKGLMSYRIITDFPSLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDY
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffact,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Sutterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LiML at: http://image.llnl.gov Series: IRAK Plate: 33 Row: h Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922334.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-UNN-2002) National Institutes of Health, Mammalian
Submitted (21-UNN-2002) National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.systemsbiology.org
context: amadan@systemsbiology.org
Anup Madan. Joesica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:21542502.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/product="MANSC domain containing 1"
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Conservative:
Mismatches:
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fissue type="Testis"
/clone lib="MIH MGC_97"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="Vector: pBluescript"
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/db_xref="LocusID:54682"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .2333
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases I to 2131)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.M. B., Bonaldo, M.F., Casavant, F.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abrameon, R.D., Willahy, S.J., Bosak, S.A., McBwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
                                                                                                                                                                                                                                                                                                                                           979 ACTCCAAAGCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACTTCTGGGACTTCC 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1039 CAGCCACAGCTGGCCACCACACCTCTGTAACCACTGTCACTTCTCACGCCTCCCACG 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1159 GCAGTTCTGACTACCACCTTTCAGGCACCTACGACACGCACCAGCAGCCAGAACCATA 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1219 CCGTTTACAGAATCTCCAACCTAACTTTGAACACAGGAATGTGTATAACCCTACTGCA 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1279 CTTTCTATGTCAAATGTGGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1339 GAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1399 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1458
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                                                                             ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
                                                                                                                                                                                                                                                                                                                                                                                                                                      261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrieulleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 LeuValLeuLeuGlyArglleLeuSerGluSerLeuArgArgLysArgTyrSerArgleu 420
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Homo sapiens MANSC domain containing 1, mRNA (cDNA clone MGC:26021
HMAGE:4824116), complete cds.
                                                                                                                                                                          GluasnvalSeralaLeuProalaThrValAlaValAlaSerProHisThrThrSerAla 240
                                                                                                                                                                                                                                          919 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 978
                                        LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro
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	RESULT 12 AB060888 LOCUS AB060888 AB060888 LOCUS DEFINITION Macaca fascicularis brain cDNA clone:QtrA-13483, full insert Sequence. ACCESSION AB060888.1 GI:13674554 KEYWORDS Oligo capping; fis (full insert sequence). SOUNCE Macaca fascicularis (crab-eating macaque) ONGANISM Macaca fascicularis BUKATYOCA; Metazzoa; Ofordata; Caniata; Vertebrata; Buteleostomi; Mammalia: Butheria: Primates; Carantalii; Cercoolthecidee;	REFERENCE (sites)  Cercopithedrane, Macaca.  (Sites)  Osada, N., Hida, M., Kuuda, J., Tanuma, R., Iseki, K., Hirai, M.,  Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.  Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.  Tibraries  JOURNAL  Unpublished  REFERENCE 2 (bases 1 to 2345)  AUTHORS Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.  TITLE  JOURNAL  JOURNAL  Lectious Diseases, Division of Genetic Resources; 23-1, Toyama  1chome, Shinjuku-ku, Tokyo 162-6840, Japan  (E-mail: khashimoin, M., Tuthp://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex.2120), Fas. 81-3-5285-1181)  COMMENT  Lab host:  COMMENT  Lab host:  Osada, N., Hida, M., Kusuda, J. and Sugano, S.  TITLE  JOURNAL  JOURNAL  Lab host:  TOPLO  COMMENT  Lab host:  TOPLO  Tel: 81-3-5285-1111 (ex.2120), Fas. 81-3-3285-1181)	Vector: pMELSS-FL3 (AGC.NO. ABOU9804) R. Sitel: DraIII (CACGTGTG) R. Sitel: DraIII (CACGTGTG) R. Sitel: DraIII (CACGTGTG) R. Sitel: DraIII (CACGTGTG) R. Sitel: DraIII (CACGTGTG) R. Sitel: DraIII (CACGTGTG) Description: 1st strand cDNA was primed with an oligo(dT) primer large specific of and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct DraIII sites of pisolate the CDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of	TORYON  CUSCOM primer used for sequencing  ( 5' end primer [CTTCTGCTCTAAAGCTGCG];  3' end primer [CGACTGCAGCTCGAGCACA] ).  Location/Qualifiers  12345  /mol_type="mRNA"  /mol_type="mRNA"  /db_xref="taxon:9541"  /clone="QtrA-13483"  /sex="male"  /tissue_type="temporal lobe right"  /dev_stage="adult"
Score: Score: Score: Score: Score: Serilarity: 99.51% Conservative: Best Local Similarity: 99.51% Mismatches: 1 Cuery Match: 6 Gaps: 10.735-014-83 (1-431) x BD227259 (1-2015) Cy 22 ArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAspIle 41 1 AGGCTGTCTGCTAGTCAGAATTGCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATC 60 Cy 42 GlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyTThrSerThrGlnGlu 61 Cy 42 GlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyThrSerThrGlnGlu 61 Ch Cy 62 AspCysIleAsnSerCysCysCysCysThrLysAsnIleSerGlyAspLysAlaCysAsnLeu 81 Ch Ch Ch Ch Ch Ch Ch Ch Ch Ch Ch Ch Ch	82 MetilePheAspThrArglysThrAlaArgGlnProAsnCysTyrLeuphePheCysPro 181 ATGATCTTCGACACTGAAAAACGTAGACCCAACTGCTACCTATTTTTTTT	142 LeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyrSer  142 LeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyrSer  143 ITACATGGCCAATTTTCACAAGCAGTCACTCCCTAGCCCATCATCACACAGATTATTCA  142 LAAGCCCATTTTCAATAGAACACACTCTCTCAGAGTTTGGATTATTCA  143 AAGCCCACCGATATTTCAATAGAACACACATTTCTCAGAATTTTGGATCCTCAGATCACACACA	Qy         222 AsnValSerAlaLeuDroAlaThrValAlalaSerProHisThrThrSerAlaThr 241           Db         601 AATGTGAGTGCGCTCCCAGGTGGCAGTTGCTTCTCCACATACCACTCGGTTACT 660           Qy         242 ProLysProAlaThrLeuLeuDroThrAsnAlaSerValThrProSerGlyThrSerGln 261           Db         661 CCAAAGCCCGCCACCCTTCTACCCACCATGCTTCAGTGACACTTCTGGGACTTCCCAG 720           Qy         262 ProGlineuAlaThrThrAlaProProValThrThrValThrValThrValThrValThrCaGGACTTCCAGGACTTCCAGGACTTCTCAGGCTCCACGAGCC 780           Db         721 CCACAGCTGGCCACCACGTGTAACCACTGTCACTTCTCAGCCTCCCAGGACC 780	Qy         282 LeuileSerThrValPheThrArgAlaAlaAlaThrIeuGlnAlaMetAlaThrThrAla 301           Db         781 CTCATTTCTACAGTTTTTACACGGGTGCGGCTACACACCAACAACAGCA 840           Qy         302 ValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePro 321           Db         841 GTTCTGACTACCACCTTTCAGGCACTCGAAAGGCAGCACTAGAACCATACG 900           Qy         322 PheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLeu 341           Db         901 TTTACAGAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCTTACTGCTT. 960           Qy         342 SerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGlu 361

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammala; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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<pre>source 12221    /organism="Homo sapiens"    /mol_type="genomic DNA"    /db_xref="taxon:9606"</pre>	Alignment Scores: 1.19e-101 Length: 2221 Score: 2022.00 Matches: 397 Percent Similarity: 92.11\$ Conservative: 0 Best Local Similarity: 92.11\$ Mismatches: 0 Query Match: 6 Gaps: 1 INS-10-735_014_83 (1.431) y HD15562 (1.2021)	1 MetPhePhedlyGluGlySerLeuThrTyrThrLeuValllelleCysPheLeuThr 1 MetPhePhedlyGluGlySerLeuThrTyrThrLeuValllelleCysPheLeuThr 266 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTG	00   004   005	101 ProbanGludladacysProbandarsGluperoscancing (1911)	464 121 524 141	Db   S84 CTCTTACATGGCCAATTTTCACAAGGCAGTCACGCCCATCATCACACAGATTAT 643     OY	201 LysGlyHisSerGlnSerSerGlnPheSerSerAstGlochagical Colinarians and light statements and ligh	Qy         241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260           Db

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                                                                                                                                                                                                                                                                                                                                                                               New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleGinSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGin
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A, Godowski PJ, Grimaldi CJ, Gurney AL;
, Napier MA, Roy MA, Tumas D, Wood WI;
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98US-0112850P.
98US-0113296P.
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Gerritsen ME, Goddard A
Hillan KJ, Kljavin IJ,
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Best Local Similarity:
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16-DEC-1998;
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Alignment Scores:

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Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
Human PRO361 nucleotide sequence SEQ ID NO:514.
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99US-0141037P.
99US-0143048P.
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                         diagnostic assay; ss.
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                                      Homo sapiens.
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22-FEB-2000;
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08-OCT-1999,
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16-DEC-1999;
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, God Grinaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paor Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Woo (GETH ) GENENTECH INC. Zhang Z;

Godowski PJ; Paoni NF; Wood WI;

WPI; 2001-032160/04. P-PSDB; AAB65299.

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.

Claim 2; Fig 327; 935pp; English

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF4400 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44200 characteric manna PRO sequences. AAF44087 to AAF44200 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

Sequence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;

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} }	, c	GluAsnCvs	TleAsnSerCvsC	veSerThrLvsAsnIle	sAsn 80
og q	406	GAAGACTGC	ATTAATTCTTGCT		
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ò	161	SerLysPro	ThrAsp11eSerT	rpArgAspThrLeuSer(	α ο
Dp	706	TCAAAGCCC	accdararcrcar	scacacacacrtrcr	cadaadiriddarccicadar 765
λ	81	HisLeuGlu	LysLeuPheLysMe	etAspGluAlaSerAla(	0
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ò.	0	LysGlyHis	SerGlnSerSerG	LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHis	LeuLeuPro 22
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ò		ThrProLys	ProAlaThrLeur	euProThrAsnAlaSer	26
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                                                               CTTTCTATGTCRAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG
                                                                                                      GAGGCCAGTCCAGGCAGTTCCTCCCAGGCAGTGTTCCAGAAAATCAGTACGGCCTTCCA
                                                                                                                                                                           LeuValleuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu
                                                  LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg
                                                                                                                                                 1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC
                                                                                            GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro
                                                                                                                                     PheGluLysTrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVallleGly
                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO361 cDNA.
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970S-006226P.
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28-MAY-1998;
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17-OCT-1997;
05-NOV-1997;
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25-FEB-1998;
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DL; Godowski PJ; Paoni NF; Wood WI; Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton Perzara N, Rong S, Gerber H, Gerittesn MS, Goddard A, Grinaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Ashkenazi AJ, Baker N, Fong S, Zhang Z;

WPI; 2003-352829/33. P-PSDB; ABU72590.

New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's disease

Claim 1; Fig 327; 663pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 201315, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma,), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases.

The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA.

The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a noyel human secreted and transmembrane PRO polypeptide 

612 A; 576 C; 464 G; 632 T; 0 U; 0 Other; Sequence 2284 BP;

2284 431 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 1.02e-141 2211.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

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140	121 ThraspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140	7
585	526 CCCAACGAGGAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT	ĸ
120	101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgllelle	н
525	466 TTGATGATCTTCGACACTCGAAAAACGACTAGACAACCCCAACTGCTACCTATTTTCTGT	4
100	81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPheCys	
465	406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGCATGTAAC	4
80	61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn	-
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09	41 IleGinSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln	·
345	286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC	Ñ
40	21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValVallleAsp	
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20	1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValllelleCysPheLeuThr	

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g	586 ACAGA	ITITCCATCTTIGACCAGAAATTIGCCAAGCCAAGAGTTACCCCAGGAAGAITCT 64
δ	141 Leule	uHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisHhrAspTyr 160
QQ Q	646 CTCT	CICTTACATGGCCAATTTTCACAAGCAGTCACTCCCTAGCCCATCATCACACAGAGTAAT 705
ò	161 SerLy	**************************************
ΩÞ	706 TCAA	GCCCACCGATATCTCATGGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765
Qy Dp	181 Histe      766 CACC	HisteuGlutysteuPheLysWetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200 
.۵	, 201 LysG	YHISSERGINSERSERGINPHESERSERASGONGLUGINILENIAHISLEULEUDRO 220
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3 8	261 Glup	•
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ζŏ	281 ThrLe	ulleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
Dp	1066 ACCC	CATTICTACAGITITITACACGGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125
ò	301 AlaV	
Db	1126 GCAG	TCTGACTACCACCTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGAAACCATA 1185
δλ	321 ProP	_
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ð í	341 LeuS	
QQ D	1246 CTTT	CTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1505
à a	361 GluA      1306 GAGG	861 GlualaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380 
ò	381 PheG	uLysTrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVallleGly 400
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Ор	w	ATTTGATCAATGGGATCTATGTGGACATC 1518
RESULT 5 ABX96832 ID ABX96 XX AC ABX96	5832	andard; cDNA; 2284 BP.
	MAY-2003	
XX DE Hu	DNA	encoding secreted/transmembrane protein PRO361.
	Human; ss; ge	ene; PRO; secreted protein; transmembrane protein;

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Cornelia de Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
diabetic complication.
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970S-0069234P.
970S-0069335P.
970S-0069425P.
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                                Homo sapiens.
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2000WO-US003565

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99WO-US030095 2000WO-US004414 2000WO-US005841 2000WO-US008439

2000WO-US014042

2000WO-US032678 001WO-US006520 2001US-00866028

GETH ) GENENTECH INC.

New transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.

Claim 2; Fig 31; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/transmembrane polypeptide (designated as PRO proteins). 15 PRO polypeptides and their encoding polynucleotides are disclosed. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, a process for producing a PRO polypeptide (by culturing the host cell under conditions for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture, an isolated polypeptide having at least 80% amino acid sequence identity to the PRO polypeptides, a chimaeric molecule comprising PRO fused to a

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AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT

LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro

201 826 221

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GluAgnValSerAlaLeuProAlaThrValAlaValAlaSerProHigThrThrSerAla

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heterologous amino acid sequence and an antibody which specifically binds to PRO. The PRO nucleotide sequences are useful as hybridisation probes, in chromosome and gene mapping, in generating sense and antisense RNA or DNA, in generating transgenic or knock-out animals which can be used in the development and screening of therapeutically useful reagents, and in gene therapy. The polypeptides may be used as molecular weight markers for protein electrophoresis purposes. The PRO polypeptides and nucleic for protein electrophoresis purposes the PRO polypeptides and nucleic RNO241 (identified as Chordin) is a candidate gene for Cornelia de Lange syndrome. Other PRO proteins are variously implicated in Immune disorders, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, cardiac injury, book organizations. The present sequence encodes a
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                   ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
                                                           GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280
                                                                                                    ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This sequence encodes a novel human secreted PRO protein
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97US-0069870P.
97US-0069873P.
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98US-0070440P.
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2001WO-US006520
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ME, Goddard A,
, Kljavin IJ,
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complications.
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Hillan KJ, Kl
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02-MAR-2000;
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28-JUL-2000;
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22-DEC-1998
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09-FEB-1998
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New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
                                                                                                                                                                                                                                                                                                                                                                                                            Gene; ss; human; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; transmembrane; antiinflammatory; anti-HIV; antiarteriosclerotic; cardiant; infertility; anti-infertility; cytostatic; antidiabetic; gene therapy; birth defect; inflammatory disease; organ failure; atherosclerosis; cardiac injury; premature aging; AIDS; cancer; diabetic complication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, an infertility, anti-HIV, cytostatic and antidiabetic activities and may
                                                           1426 CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG
1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC
                                    LeuValLeuLeuGlyArgileLeuSerGluSerLeuArgArgLyaArgTyrSerArgLeu
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Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney .
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood W
                                                                                                                 cDNA encoding human PRO361 protein.
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                                                                                                                                                                                                                                             ABX77120 standard; cDNA; 2284
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98WO-US025108.
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P-PSDB; ABU57251.
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28-FEB-2001;
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                                                     11eGinSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln
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  GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr
                                                 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr
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diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy;
tumour-associated antigenic target; TAT; ADBET;
antibody-dependent enzyme mediated prodrug therapy; cytostatic.
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25-FEB-1998;
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used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a nucleic acid sequence of the invention
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The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bloactive molecules to cells expressing PRO polypeptides, for modulating collogical activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists. The polynucleotide sequences cromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of RRO polypeptides, for generating transgenic animals or knockout animals, to construct hybridisation probes for mapping the construct hybridisation probes for mapping the construct hybridisation probes for can individuals with genetic disorders, and for the genetic animals of individuals with genetic disorders, and for genetating probes for PCR, construct animalysis, Southern analysis and Western analysis. The present sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequeta.uspto.gov/psipsDIDEntry.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses.
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Godowski P.
Paoni NF;
Wood WI;
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                                                                                                                                                                                                                                                                                                               Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton I Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, I Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 2284 BP; 612 A; 576 C; 464 G; 632 T; 0 U; 0 Other;
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30-MAY-2000; 2000MO-US014941.
28-JUL-2000; 2000MO-US015264.
28-JUL-2000; 2000MO-US022031.
11-AUG-2000; 2000MO-US023522.
23-AUG-2000; 2000MO-US023522.
24-AUG-2000; 2000MO-US03326.
01-DEC-2000; 2000MO-US0332678.
01-DEC-2000; 2000MO-US032678.
01-UN-2001; 2001MO-US017860.
20-JUN-2001; 2001MO-US019692.
29-JUN-2001; 2001MO-US01966.
09-JUL-2001; 2001MO-US01735.
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ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405
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                           GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn
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                                               GAAGACTGCATTAATTCTTGCTGTTCAACAAAAACATATCAGGGGGACAAAGCATGTAAC
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Human; 88; gene; PRO; antiinflammatory; antiarteriosclerotic; cardiant; yprecological; anti-HTV; cytostatic; antidiabetic; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; acquired immunodeficiency syndrome.
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,, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                                                                          Human cDNA encoding secreted/transmembrane protein, PRO361
AspryrLeuileAsnGlyileTyrValAspile 431
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98US-0113296P.
99WO-US012252.
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99WO-US021090.
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2000WO-US014042.
2000WO-US020710.
2000WO-US032678.
2001US-00866028.
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98WO-US025108
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2000WO-US005841
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Hillan KJ, Kljavin IJ,
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P-PSDB; ABU56315.
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30-NOV-1999;
10-DEC-1999;
11-FBB-2000;
22-FBB-2000;
30-MAR-2000;
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30-MAR-2000;
30-MAR-2000;
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28-JUL-2000;
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28-JUL-1999;
15-SEP-1999;
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01-DEC-1998;
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25-FEB-1998;
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New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic complications

Claim 2; Fig 31; 171pp; English

The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to and scoring at least 80% positives when compared to any of 15 fully defined sequences of 235-954 amino acids, given in the specification. Also included are: (1) an isolated PRO circluded are: (1) an isolated PRO control of the specification and enclosed are: (1) an isolated PRO control of comprising any of 15 fully defined nucleotide sequences of 957-3441 bp. Comprising any of 15 fully defined nucleotide sequences of 957-3441 bp. Comprising the Rectar and deposited under ATCC accession number are comprising the PRO nucleic acid; (3) a host cell comprising the vector. Comprising the PRO nucleic acid; (3) a host cell comprising the vector; (4) producing PRO polypeptides, comprising culturing the cell for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture; (5) a chimaeric molecule comprising PRO polypeptide and recovering the PRO polypeptide and compression are useful for the diagnosis and treatment of methods and compositions are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS comprised and compositions are useful cancer, diabetic complications and mutations in general. The present sequence is a cDNA encoding a PRO control of the procession of the present sequence is a cDNA encoding and processing the present sequence is a cDNA encoding and processing the present sequence is a cDNA encoding and processing the present sequence is a cDNA encoding and processing the processing the present sequence is a cDNA encoding and the present sequence is a cDNA encoding and the processing the present sequence is a cDNA encoding and the present sequence is a cDNA encoding and the present sequence is a cDNA encoding and the processing the present sequence is a cDNA encoding and the present and the present as the present and the present as the present and th polypeptide 

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LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160 286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGAC 345 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120 ThraspPheProSerLeuThrargasnLeuProSerGlnGluLeuProGlnGluAspSer 140 CICITACATGGCCAATITICACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705 1 MetPheDheGlyGlyGluGlySerLeuThrTyrThrLeuValllelleCysPheLeuThr 20 GludspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 41 IleGinSerSerLeuSerLysGlyIleArgGlyAsnGluDroValTyrThrSerThrGin 346 ATCCAGTCATCTTTTTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTCTGT CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGGCCAAGAGTTACCCCAGGAAGATTCT 21 LeuArgleuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValVallleAsp GAAGACTGCATTAATTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC 2284 431 0 0 0 Length:
Matches:
Conservative:
Mismatches:
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lnLysPheGlySer( 	InteuteuAlaTyri                  AGCTCCTTGCTTAT/	luIleAlaHisLeul 	erProHisThrThr( 	alThrProSerGly                TGACACCTTCTGGG	alThrSerGlnProl              TCACTTCTCAGCCT	euGlnAlaMetAla'              TCCAAGCAATGGCTV	ysGlySerLeuGlu' 	snValTyrAsnPro:                        ATGTGTATAACCCT	hralaserTrpglu( 	luasnglnTyrglyl                   AAATCAGTACGGC	alleuPheleuVal] 	gArgLysArgTyrSer/	100116					otein PRO361.	ue typing; gene ; organ failure th defect; me; AIDS; cance oteoglycan rele rtilage defect;	
eSertrpargaspthrLeuSerGlnLysPheGlySerSerasp 	repglualaSeralag 	heserseraspglng                   "TTTCCTCTGATCAAG	hrvalAlavalAlas 	rothrasnalaServ               :ccaccaatGcttcaG	roProvalThrThrv                CACCTGTAACCACTG	rgAlaAlaAlaThri              :GGCTGCGGCTACAC	laProThrAspSerL 	hrLeuAsnThrGlyA                  CTTTGAACACAGGGA	erThrMetAsnLysT                  CCACTATGAATAAAA	ilnglyServalProg 	erLeuLeuPheGlyV	leLeuSerGluSerLeuArgA	, 4					transmembrane pr	tride, PRO; tiss nmatory disease nfertility, bir ficiency syndro em disorder; pr in, articular ca	
fhraspileserfrp <sup>2</sup> 	HisteuGlutysteuPhetysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 	LygdlyHisSerglnSerSerglnPheSerSerAspglnGlulleAlaHisLeuLeuPro 	GluasnvalSeralaLeuProalaThrvalAlavalAlaserProHisThrThrSerala 	Thr ProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 	GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 	hrleuileSerthrValPhethrArgAlaAlaAlaAlathrleuglnAlaMetAlaThrThr 	AlaValieuthrthrthrpheginalaprothraspseriysgiyserleugluthrill 	ProPheThrGlu11eSerAanLeuThrLeuAanThrGlyAanValTyrAanProThrAla 	Leusermetserarnvalgluserserthrmetarnivsthralasertrpgluglyarg 	Glualaserproglyserserserginglyservalprogluaenginfyrglybeupro 		LeuValLeuLeuGlyArgileLeuS	[leAsnGlyIleTyr\	ATTTGATCAATGGGATCTATG	CDNA; 2284 BP.		entry)	l secreted and t	Secreted and transmembrane polypeptide; PRO; tissue typing; transgenic; knockout animal; inflammatory disease; organ fai athersoslerossis; cardiac injury; infertility; birth defect; premature aging; acquired immunodeficiency syndrome; AIDS; or diabetic complication; immune system disorder; proteoglycan sports-related joint problem; human; articular cartilage defi	
SerLysProThrAsp11	HisLeuGlul          CACCTGGAGA	Lysglyhis6          AAAGGCCAT7	GluAsnVals	ThrProLys!	GlnProGlnI            CAGCCACAGG	ThrLeuile(	AlavalLeu1          GCAGTTCTG1	ProPheThr(            CCGTTTACA(	LeuSerMets             CTTTCTATGT	Glualaser           GAGGCCAGTO	PheGluLys1	LeuvalLeul	AspTyrLeu	GATTATTE	standard;		(Ei	oding novel	and transmic; knockoulerosis; calerosis; cale aging; accomplicatielated joir	
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therapy. (II) is also useful for generating transgenic animals or knockout animals for the development and screening of therapeutically useful reagents. PRO213 polypeptide is useful for treating inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer and diabetic complications. The other PRO polypeptides including PRO243, PRO323, PRO327, PRO344, PRO347, PRO354, PRO355, PRO15, PRO561 and PRO355, PRO415, PRO541 is useful for treating human disorders involving the immune system. PRO41 is useful for stimulating release of proteoglycans from cartilage, and thus for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. (I) is also useful for inhibiting vascular endothelial cell growth factor (VEGF) stimulated proliferation of endothelial cell growth. This sequence encodes a novel human secreted and transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGGGTCTAGAAGAGTGTTGTCATTGAC 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated PRO polypeptides e.g. PRO243, PRO299, PRO323, PRO327, PRO344, and polynucleotides useful in the treatment of human disorders related to immune system, and in gene therapy.
 osteoarthritis; rheumatoid arthritis; vascular endothelial cell growth factor stimulated proliferation; endothelial cell growth; VEGF stimulated proliferation; gene; ss.
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,, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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Geritsen ME, Goddard A, Godowski
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               CTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG
GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT
                                                                                                                  AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle
                                                                                                                                                   ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla
                                                                                                                                                                                   LeuSerMetSerAsnValGluSerSerThrMetAsnlvysThrAlaSerTrpGluGlyArg
                                                                                                                                                                                                                     GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro
                                                                                                                                                                                                                                                       PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly
                                                                                                                                                                                                                                                                 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC
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                                                                                                                                                                                                                                                                                                                        ABX79658 standard; cDNA; 2284 BP
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25-FEB-1998;
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The invention discusses isolated two secreted transmembrane polypetities comprising a sequence without signal peptide and the mucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX79290-ABX79675 are the genes encoding, the primers presented in ABX79290-ABX79675 are the genes encoding, the primers propes detecting the PRO polynucleotides of the invention. Note: The sequence date for this patent is also available in clearing format from USPTO at sequata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses isolated PRO secreted/transmembrane polypeptides
                                                                                                                                                                                                                                                                                                                                                         Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers.
                                                                                                                                                                                                                                                                                                                                                                                  Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Perrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
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                                                                08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US017800.
01-JUN-2001; 2001WO-US017800
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P-PSDB; ABU59045.
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Best Local Similarity:
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2284 431 0 0 0 Length:
Matches:
Conservative:
Mismatches: Gaps: 1.02e-141 2211.00 100.00% 100.00% Query Match:

US-10-735-014-83 (1-431) x ABX79658 (1-2284)

MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr 20

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	21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40	286 CTAAGGCTGTTGTTGTTGTGTGTGTGTGTGTGTGTGTGTG	41 IleGlnSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln 60	346 ATCCAGTCATCTTTTTTAAGGGAATCAGAGCCAATGAGCCCGTATATACTTCAACTCAA 405
	LeuArgLeuSerAlaS	CTAAGGCTGTCTGCTA	IleGlnSerSerLeuS	ATCCAGTCATCTCTTT
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	3dAddatrcT 645 3Thraspty 160 ACAGATTAT 705 SerSerasp 180               ATCCTCAGAT 765 ATCTCAGAT 765 TYTLYBG1U 200				CGCCTTCCA 1365 CGCCTTCCA 1365 SGTGATAGGC 1425 GGTGATAGGC 1426 TCAAGACTG 1485 TCAAGACTG 1485
ACCAACTICTACCT. ACGIVEUMETSETTY. ACGACTTATGACTTACCT. ACGACTTATGACTTA.	86 ACAGAITTTCCATCTTGACCAGAATTTGCCAAGACTTACCCCAGGAAGATTT 645 41 LeuleuhisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisHisThrAspTyr 160 46 CTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCCTAGCCATCATCACACAGATTAT 705 61 SerLySProThrAspIleSerTrpArgAspThrLeuSerGlnLySPheGlySerSerAsp 180 65 TCAAAGCCCACCGATTTCATGAGAGACACATTTCTCAGAAGTTTGGATCCTCAGAT 765 61 TAAAGCCCACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765 62 TCAAAGCCCACCGATATCTCATGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT 765 63 HisLeuGluLySLeuPheLySMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLySGlu 200 64 CACCTGGAGAAACTATTAAGATGAATGAAGTGCCCAGCTCCTTGCTTATAAGGAA 825	ppglnglullealatii 			TCCAGAAATCAGTA TCCAGAAAATCAGTA TGGTGTCCTGTTCCT TAGTGTCCTGTTCCT TAGTGTCCTGTTCCT TGGTGTCCTGTTCCT TGGTGTCCTGTTCCT TGGTGTCCTGTTCCT TCCCCGGGAAACGTTA
MAAAACAGCTAGACA MAAAACAGCTAGACA OoleuLysProhlaly ATTGAAACCAGCAAA TATGAAACCAGCAAA	CAGAAATTTGCCAAG rcGaAAATTTGCCAAG rcGaAGCAGTCACTCC rTTPARGASTARTE                   rTGAGAGAGACACTC rangasgaCACACTCCACTCGAGAGAGACACACTCACTCGAGAGACACACTCACT	rglnPheserSerAs ACATTTCCTCTGA coAlaThrValAlaVa [              ACTACGGTGCACI ACTACGGTGCACI WLeuProThrAsnAl	uralaproprovalth "AGTCCACCTGTAAC EThrargalaalaal "HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	nleuThrLeuAsnTh	CTCCCAGGCAGTGT eGlySerLeuleuPh
TGATCTTCGACACTCC SnGludluAlaCysPr ACGAGGAAGCCTGTC SpPheProSerLeuTP	ALTITICALCITITION  EUHISGLYGIPHESE	1ytisserginserse 	roglnLeualathrth [	heThrGlulleSerAs 	
466 TTGA 101 ProAc 526 CCCAL 121 ThYAC	. 586 ACAGIA 141 Leule 646 CTCT 161 Serfy 706 TCAAA 181 Hisle 766 CACC	201 LysG;             826 AAAGG 221 Glua   886 GAAAG 241 ThrPh 946 ACTCC	261 GlnP 1006 CAGCC 281 Thric 1066 ACCCC 301 AlaVa 1126 GCAGF		1306 GAGG 381 PheG 1366 TTTG 401 LeuV

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                                                                                                                   Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185; PRO943; PRO113; PRO313; PRO1387; PRO363; PRO5723; PRO1114; PRO3301; PRO940; PRO1181; PRO7170; PRO361; PRO846; bioactive molecule; toxin; radiolabel; antibody; call issue typing; gene therapy; cytostatic; chromosome mapping; gene mapping; transgenic animal; knockout animal; immunohistochemical staining; gene; ss.
                                                                                                    Novel human secreted and transmembrane protein PRO361 cDNA
          1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
421 AspTyrLeuIleAsnGlyIleTyrValAspIle 431
                                                  ACA93679 standard; cDNA; 2284
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970S-0062250P-
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980S-0081322P-
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226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285	JLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValVe	286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAAGATGTTGTCATTGAC 345	SerSer[.e.]\		346 ATCCAGTCATCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA 405	61 GluAspCys1leAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80	4 0 6 Gab Gab Charles a minimum Carama a mana minimum Carama a Car		81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100	ITCTTCGACACTCGAAAACAGCTAGACAACCGAACTG		12	526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585				ACAGALITICCALCITIGACCAGAMITIGCCAAGCCAAGAGITACCCCAGGAAGATICI	lyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 1		GCCAATTTTCACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 7	161 SerivsProThrAsnIleSerTrnAraAspThrLeuSerGlnLvsPheGlvSerAsp 180		706 rcaaadcccaccgararcrcarggagagacacacrrrcrcagaagrriggarccrcagar 765	101 ພະນຸ ພາກ ເປັນ ເປັນ ທ່ານ ການ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປັກພາກ ປ	nisheudiunysheurijehysmechspoluhiaaagiineduleuniaiyinysoiiu z	766 CACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCAGCTCCTTGCTTATAAGGAA 825	201 IvsGlvHisSerGlnSerSerGlnPheSerSerAsnGlnGluIleAlaHisLeuLeuPro 220		826 AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885	221 GludanValSeralaLeuDroalaTaThrValalaJaSerDroHisThrThrSerala 240		886 GAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT 945	241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260		946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005	261 GlnProGlnLeuAlaThrAlaProProValThrValThrSerGlnProProThr 280		CAGCCACACACCACACCACAGCICCACCIGICACIICICACIICACCICCCACG	281 ThrieulleSerThrValPheThrArgAlaAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300	1066 10 10 10 10 10 10 10 10 10 10 10 10 10		301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320	TGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTT	321 PropheThrGlulleSerAsnLeuThrLeuAsnThrGlvAsnValTvrAsnProThrAla 340		l'CCAACTTAACTTTGAACACAGGAATGTGTATAACCCTACTGCA	341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360	1246 CTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCCTGGGAAGGTAGG 1305
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18-AUG-1998;	19-AUG-1	20-AUG-1 24-AUG-1	26-AUG-1 26-AUG-1	26-AUG-1	26-AUG-1 26-AUG-1	26-AUG-1	26-AUG-1	26-AUG-1	31-AUG-1	16-SEP-1	17-SEP-1	17-SEP-1	01-DEC-1	22-DEC-1	05-JAN-1	20-FEB-1	12-MAR-1	02-JUN-1	23 - JUN - 1	07-JUL-1	26-JUL-1	28-JUL-1	17-AUG-1	15-SEP-1	08-0CT-1	30-NOV-1	01-DEC-1	16-DEC-1	05-JAN-2	11-FEB-2	18-FEB-2	22-FEB-2	24-FEB-2	02-MAR-2	15-MAR-2000	20-MAR-2	30-MAR-2000;	17-MAY-2	22-MAY-2000	30-MAY-2000	23-JUN-2000	28-JUL-2		Alignment Sco Pred. No.:	Score:	Percent Similarity: Best Local Similarity	Query Match:	

1 MetPhePheGlyGlyGlyGlySerLeuThrTyrThrLeuVall1eIleCysPheLeuThr 20

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  1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC 1425
                                            400
                                                                                                                                                                                                             Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; endothelial growth factor inhibition; VEGF inhibition; endothelial growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; chamatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
         PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly
                                                                                                                                                                                            Novel human secreted or transmembrane protein PRO846 DNA.
                                                                                ABX81361 standard; DNA; 2284 BP
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  1186 CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA 1245
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                341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg
                          GluAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro
                                                          PheGluLysTrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVallleGly
                                                                                             1366 TTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCCTGGTGATAGGC
                                                                                                                                                                                                                                                         Novel human secreted and transmembrane protein PRO361 cDNA
                                                                                                                                                   ACA93177 standard; cDNA; 2284 BP
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1 MetPhePheGlyGlyGlySerLeuThrTyrThrLeuValIleIleCysPheLeuThr

Length: Matches: Conservative: Mismatches: Indels:

1.02e-141 2211.00 100.00\$ 100.00\$

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores: Pred. No.:

2000WO-US015264. 2000US-0213637P. 2000WO-US020710. 2000WO-US022031. 2000WO-US023522.

02-JUN-2000; 23-JUN-2000; 28-JUL-2000; 11-AUG-2000; 23-AUG-2000;

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Gaps:

US-10-735-014-83 (1-431) x ACA93177 (1-2284)

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LeuLeuhisGlyGlnPheSerGlnAlaValThrProLeuAlahisHisHisThrAspTyr 160

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SerlysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180

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LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlulleAlaHisLeuLeuPro

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826 221 886 241 946 261 1006 281

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GAAAATGTGAGTGCGCTCCCCAGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCT

GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrSerAla

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ThrLeulleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300

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Search completed: April 26, 2005, 22:36:16 Job time : 632 secs

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Sequence 340, App
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CURRENT FILING DATE: 2001-05-25
FILE SEPLICATION DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 82
                                                                                                                                                                   Sequence 1.
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US-09-949-016-17361

US-09-370-838-158

US-08-323-1708-1

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US-09-614-221A-91

US-09-614-221A-91

US-09-437-054A-7

US-09-437-054A-7

US-09-326-467A-3

US-09-326-467A-3

US-09-326-361B-4

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 82, Application US/09866028
Sequence No. 6642360
GENERAL INFORMATION
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.97e-217
                    Roy, Margaret
Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Napier, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eaton, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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US-09-866-028-82
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APPLICANT:
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CgnZ_1/USFTO_spool p/US10735014/runat_26042005_113101_7446/app_query.fasta_1.583
-Q=/CgnZ_1/USFTO_spool p/US10735014/runat_26042005_113101_7446/app_query.fasta_1.583
-D=16sued_Patente NA -QFMT=fastap -SUFFIX=rni -MINATCH=0.1 -LOOPCJ=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_NAX=100 -THR_NITS=0 -ALIGN=15
-MODE=LCAL -OUTFNT=pto -NORM=ext -HEAPPIZE=500 -MINLEN=0 -MXLEN=200000000
-USER=US10735014 @CGN_1 1_105 @runat_26042005_113101_7446 -NCPU=6 -ICPU=3
-NO_MARP -LARGEQUERY -NEG_SCORE=0 -WAIT -DSPBILOK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREAPS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13892, A Sequence 950, App Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 15, Appli Sequence 12147, A
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Sequence 412, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 82, Appl
Sequence 82, Appl
                                                                                                            April 26, 2005, 22:02:22 ; Search time 223 Seconds (without alignments) 3162.490 Million cell updates/sec
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                                                                                                                                                                              US-10-735-014-83
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1 MFFGGEGSLTYTLVIICFLT......LRRKRYSRLDYLINGIYVDI 431
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Sequence
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1: /GgT2_6/prodata/1/ina/5A_COMB.seq:*
2: /GgT2_6/prodata/1/ina/5B_COMB.seq:*
3: /GgT2_6/prodata/1/ina/6A_COMB.seq:*
4: /GGT2_6/prodata/1/ina/6B_COMB.seq:*
5: /GGT2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /GGT2_6/prodata/1/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                   nucleic search, using frame_plus_p2n model
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US-09-944-457-82
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US-09-480-8477-0
US-09-774-528-230
US-09-774-528-230
US-09-949-016-13892
US-09-949-016-13892
US-09-241-581B-5
US-09-26-26-5
US-09-95-07721-5
US-09-949-016-12147
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Xgapop 10.0 ,
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152
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Database

Result No.

	rProdlySerSerSerGlnGlySerValProGluAsnGlnT 	381 PheGlulysTrpLeuleulleGlySerLeuleuPheGlyValLeuPheLeuVallleGly	401 LeuValLeuleuGiyArgileLeuSerGluSerI 	Oy 421 AspTyrLeuIleAenGlylleTyrValAspIle 431 	RESULT 2 US-09-944-457-82 ; Sequence 82, Application US/09944457 ; Patent No. 6734288	; GENERAL INPORMATION: ; APPLICANT: Baker, Kevin ; APPLICANT: Botstein, David ; APPLICANT: Eaton, Dan		; APPLICANT: Godowski, Paul ; APPLICANT: Grimaldi, Christopher ; APPLICANT: Gurney, Austin ; APPLICANT: Hillan, Kenneth	; APPLICANT: Kljavin,Ivar ; APPLICANT: Napier,Mary ; APPLICANT: ROY,Margaret ; APPLICANT: Tumas,Daniel	; APPLICANT: WOOD, WILLIAM ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ; TITLE OF INVENTION: ACIDS ENCODING THE SAME ; FILE REFERENCE: P2548PIC1	CURRENT APPLICATION NUMBER: US/09/944,457 ; CURRENT FILING DATE: 2001-09-26 ; PRIOR APPLICATION NUMBER: 09/866,028 ; PRIOR FILING DATE: 2001-05-25						; PRIOR APPLICATION NUMBER: 60/068,017 ; PRIOR FILING DATE: December 18, 1997
e: 2211.00 Matches: ent Similarity: 100.00\$ Conservati Local Similarity: 100.00\$ Mismatches Y Match: 100.00\$ Indels:	US-10-735-014-83 (1-431) x US-09-866-028-82 (1-2284) Qy	eralaSerGlnAsnCysLeuLysLysSerLeuGluAspVe 	Qy 41 IleGlnSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln 60	AspC      GACT	Qy 81 LeumetilePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100	Qy     101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArg11e11e 120       Db     526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585	Oy 121 ThraspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140	Qy       141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisHixBpTyr 160         Db       646 CTCTTACATGGCCAATTTTCACAAGGAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705	Qy 161 SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180	Qy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200	Oy 201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro 220	Qy 221 GludsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240	Qy       241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260         Db       946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC 1005	Oy 261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280	Oy 281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300	Qy     301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle     320       Db     1126 GCAGTTCTGACTACCACCTTTCAGGCACTACGGACTCGAAAGGCAGCTTAGAAACCATA     1185	Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340

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CITICIAIGECAAAIGEGGGGGCCTTCCACTATGAAIAAAACTGCTTCCTGGGAAGGTAGG 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1066 ACCCICATITCTÁCAGITITITACACGGCTGCGGCTACACTCCAAGCAATGGCTACAACA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluAlaSerProGlySerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380
                                                                                                                                                                                                                                                                                                                                                            ProbsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArglle11e 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 ATCCAGTCATCTCTTTCTAAGGGAATCAGAGGCAATGAGCCCGTATATACTTCAACTCAA
                                                                                                                                                                                    GluAspCys1leAsnSerCysCysSerThrLysAsn1leSerGlyAspLysAlaCysAsn
                                                                                                                                                                                                                                                                        LeuMetIlePheAspThrAzgLysThrAlaAzgGlnProAsnCysTyrLeuPhePheCys
                                                                                                                                                                                                                                                                                                                                                                                                         526 CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGAGTTACCCAAGAGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCCAGCTCCTTGCTTATAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGGAATGTGTATAACCCTACTGCA
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                                          286 CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAAGAGTCTAGAAAAGATGTTGTCATTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SertysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCTCAGAAGTTTGGATCCTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HisteuGluLysteuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        886 GAAAATGTGAGTGCGCTCCCCAGCTACGTGCTTCTTCCACATACCACCTCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         946 ACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACCTTCTGGGACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1006 cagcicacaderedecadeaceaceaceretratecaceaceaceaceaceace
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               21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp
                                                                                                 41 IleGlnSerSerLeuSerLysGlyIleArgGlyAsnGluProValTyrThrSerThrGln
                                                                                                                                                                                                                               406 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAACATATCAGGGGACAAAGCATGTAAC
                                                                                                                                                                                                                                                                                                                   466 TIGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thraspphe ProSerLeuThrargasnLeuProSerGlnGluLeuProGlnGluAspSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr
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                                                                                                                                                                                       61
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PRIOR APPLICATION NUMBER: 60/070,440
PRIOR PILING DATE: January 5, 1998
PRIOR FILING DATE: February 9, 1998
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PRIOR PLING DATE: December 16, 1998
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PRIOR PLING DATE: PEDTUARY 11, 2000
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                                                            LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
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; Sequence 9897, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Duclart, A.
; APPLICANT: Duclart, A.
; APPLICANT: Duclart, A.
; APPLICANT: Duclart, A.
; Patent No. 6783961
; FILE REFERENCE: 5.9.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR PAPLICATION NUMBER: US 60/122,487
; PRIOR PAPLICATION NUMBER: US 60/122,487
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LOCATION: 58
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LOCATION: 59
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LOCATION: 136
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LOCATION: 69
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NAME/KEY: misc_feature
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LOCATION: 126
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289 AGCATCYCCTTAGCAGCCGCTCTGATCCCTTGGCCAAGCAG---GAGGGAACCATTAGC 345
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Patent No. 6476195
GENERAL INFORMATION:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
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Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aldong J.
Wehrman, Tom
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Wang, Dunrui
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; LOCATION: (415)..(1764)
US-09-774-528-230
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                        Sequence 230, Applic
Patent No. 6743619
GENERAL INFORMATION:
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973 CTCAGCACACACCCTCGCACAAGAGCAGCAGCGCGTTGCCAAGAACAGCAACCCTG 1032
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   CACCCACAAGATGTGGACAGCTCTTGTGCTCATTTGGATTTTYTCCTTGTCCTTATCTGA 462
                                                                                            LeuPhePheCysProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeu---- 114
                                                                                                                                                                                                                      SerTyrArgIleIleThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeu 135
                                                                                                                                                                                                                                                                                 136 ProGlnGluAspSerLeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHis 155
                                                                                                                                                                                                                                                                                                                                             156 HisHisThrAspTyrSerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLys 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                      697 GGAGGIGCAGCIGAIGGIGIGACCICCAIIGCICCCACGGCIGIGGCCICCAGIACGACI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 LeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIle 215
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                                                                                                                           ----CAACTTTGTCCCTAACAAATGTGGAAGGGATTAGTCAA
                                                                                                                                                                                      529 GAGGAATGCATCTGTGGAAACAGTTGATAATAAAACGTCTGAGGATGTAACCATGGCAGC
                                                                                                                                                                                                                                                   589 AGCTTCTCCTGTCACATTGACCAAAGGGATTCGGCAGCCCAMCTCAACTCTATGGAAGTC
                                LysAlaCysAsnLeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 ThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla----
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                                                    664 AGCAGGACAGATGTGAGTGAACCA----
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1321 ACCCTTTTCATCACAGTCTTGGTTTTGTTTGCCTGCAGGCCTATGAGAGCTACAAGAAG 1380
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ENTION: No. 6743619el Nucleic Acids and
ENTION: Polypeptides
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Matches:
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TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
                                                                                                                                                                                                   Application US/09774528
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SOFTWARE: pt_FL_genes Version 2.0
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; TYPE: DNA ; ORGANISM: Human US-09-949-016-13892 Alignment Scores:	10-735-014-83 (1-431) x US-09-949-016-13892 (1-1656)  22 ArgleuSerAlaSerGlnAsnCysLeuLysLysSerLeuC			Db 6664 TGTGGTGAĊCTCTTĊTĊAĀAĠACTGCGGGTCCCAACACCCCCCCAGATTTTCCCATTTC 6723  Qy 177 ySerSerAspHisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAl 197  Db 6724 TCTGGGCTCTCATCTTGCATCTTACATCAGAGTTCTTTTGGTTCTGTCCAACTTTTAGG 6783  Qy 197 aTyr
167   SerTrp		454 TCTTGGCAGAAATCCAGGACAACCAGCACCTCCATCLALLINI	341 LeuSerNetSerAanValGluserSerThrMetAanLysThrAlaSerTrpGluGlyArg 360 754 AccAGCACAACCCCTACAAGCACACACCTCCACCACACACACA	ENERAL INFORMATION: APPLICAMY: VENTURE, APPLICAMY: VENTURE, APPLICAMY: VENTURE, APPLICAMY: VENTURE, APPLICAMY: VENTURE, APPLICAMY: VENTURE, APPLICAMY: VENTURE: APPLICAMY: VENTURE: APPLICATION NUMBER: US/09/949,016 CURRENT PILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03 PRIOR PLILING DATE: 2000-10-03 PRIOR PLILING DATE: 2000-10-03 PRIOR PLILING DATE: 2000-10-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 13892

8 8 8

Db 367 CCAACACTCACGAGCGAGCTGTCCACCTCTCAGGCCGAGAACCAGCAC 414  Qy 144 GlyGlnPheSerGlnAlaValThrProLeuAlaHisHisThrAspTyrSerLyB 162  Db 415 GCCCAGGACAGAGACGACAATGACCCTTGACTAACACCACCACCAGGGACGAC 474  Qy 163 ProThrAspIle-SerTrpArgAspThrLeuSerGlnLySPhe 176	Db 475 ¢¢¢¢crgrcaA¢¢¢aAgrgrgaqrgʻqéaCagaGrrrgacGrgaCrrcaA¢G 534 Qy 177GlySerSerAspHisLeuGluLySLeu	Qy         186	Qy 190 uAlaSerAlaGlnLeuLeuAlaTyrLysGluLysGlyHisSerGl 205	Oy 205 nSerSerGlnPheSerSerAspGlnGlulleAlaHisLeuLeuProGluAsnVa 223	Qy 223 ISerAlaLeuProAlaThrValAla8erProHisThrThrSerAlaThrProLy 243	243 835	Oy 261 nProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThrTh 281 :::	Qy 281 rLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrAl 301 :::::::	Oy 301 aValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIlePr 321	Qy 321 oPheThrGluileSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAlaLe 341 ::: Db 1027 AGCACTGAGAAGCCACCACCACACCCACAGCTAC 1062	Oy 341 uSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArgGl 361	Qy 361 uAlaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTy 377 :::               :::::::::::::::::	377 x 377	Db 1183 C 1183	1581B	ass BI and CI	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Patrea L. Pabst ; STREET: 2800 One Atlantic Center
Oy 243 sProAlaThrLeuLeuDroThrAsnAlaSerValThrProSerGlyThrSerGlnDroGl 263	281 rLeu	<pre>Qy 292 aThrLeuGlnAlaMetAlaThrThrAlaValLeuThrThrThrThrPheGln 308  Db 7138 GGTGACTAACCCCTGTACAATTGCTGCAGCACCTACTACTACTTGAGGTACTACTTG 7197  Ov 309AlaProThrAspSerLvgGlvSerLeuGluThr11e 320</pre>			Db 7318 GATACCAGTCTCCTCCTCTGCAGACCCTGAAGACCTCAAAAATCTCCCCAGTTCAGT 7377	350 rMetAsnLysThralaSerTrpGluGlyArgGluAlaSerE 7378 ATTGGTTAATTTCCAACACAAAAAGACTCCAAACTGTAC		RESULT 8  US-05-594-950 ; Sequence 950, Application US/09976594 ; Patent No. 6673549	APPLICANT: FULLDES, Michael ; APPLICANT: Buchbinder, Jenny ; TITLE FOR INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS	; FILE KEFKENCE: PA-0011 US ; CURRENT APPLICATION NUMBER: US/09/976,594 ; CURRENT PILING DATE: 2001-10-12 ; PRIOR APPLICATION NUMBER: 60/240,409		tryPi Dravin: 129/ TryPi Dra Organism: Homo sapiens Frature:	; NAME/KEY: misc_feature ; OTHER INFORMATION: Incyte ID No. 6673549 1328310.1 ;; A9-976-594-950	ignment Scores:	Pred. No.: 1.71e-05 Length: 1297 Score: 152.00 Matches: 65 Percent Similarity: 38.21% Conservative: 50 Best Local Similarity: 21.59% Mismatches: 111 Ouery Match: 6.87% Indels: 75		Oy 124 ProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSerLeuLeuHis 143

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1298 CTACTACAACTACAACTAAAAGGCCAACCACAACAACAACAACAACAAAGGCCA 1357
                                                                                                                                                       1358 CAACTACAAAGGGAACAACAACCACTAAAAAACCGACAACAACATCAACAACGCGGAAGC 1417
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|1565 CAGGCATC-----ATCACCACCATGAAGACACGCAAGCGCATCACTTGGAACG 1612
                                                                                                                                                                                                                                                1418 caacaacaacgactrcaaccaccaaagrcracaactrcracaacgrcracaactrcaa 1477
                                                                                                                                                                                                                                                                                                                                                                                                                         1525 --------ACAACAATAATGATCCCTACTTCCGGAAAGACTA 1564
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                                                                                                                                                                                                                                                                                             299 hrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 hrAlaLeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrp---- 357
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                         239 erAlaThrProLygProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyT
                                                                                                                                                                                                      roThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaT
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                                                                                                             hrSerGlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProP
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Patent No. 6429289
GENERAL INFORMATION:
APPLICANT: Krieger, Monty
TITLE OF INVENTION: Class BI Scavenger Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,428
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,3
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ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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1673 TAGTA---
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US-08-265-428-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 eSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAspHisLeuGluLysLeuPh 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ThrS 239
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                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1926 encode the amino acid sequence
201 West Peachtree Street
                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for the Drosophila Melanogaster
Scavenger Receptor Class CI."
NCE DESCRIPTION: SEQ ID NO: 5:
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TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2032 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc. feature
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OTHER INFORMATION:
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23.47%
6.69%
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                        ZIP: 30309-3450
                                            Georgia
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Best Local Similarity:
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1926 encode the amino acid sequence
for the Drosophila Melanogaster
Scavenger Receptor Class CI."
                                                                                                                                                                                 Sequence 5, Application PC/TUS9507721
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Class BI and CI Scavenger Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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                                                                                     ----GTACTTTACCTGCTACTCGGCATTGTTCTGGTG 1710
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SURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07721
FILLING DATE:
CLASSIFICATION:
NAME: Pabet, Patrea L.
NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
                                                             392 heGlyValLeuPheLeuValIleGlyLeuValLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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23.47$
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STRANDEDNESS: double
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OTHER INFORMATION:
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MOLECULE TYPE: CD
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1673 TAGTA-
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US-08-265-428-5
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                 MOLECULE TYPE: CDNA
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Sequence 12147, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12147
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Query Match:
TYPE: DNA
ORGANISM: Human
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 erProHisThrSerAlaThrProLysProAlaThrLeuLeuProThrAsnAlaSerV 254
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                                                                          alThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr----
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APPLICANT: Mohamath, Roadoh
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.475c1
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-04-02
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
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JAPELICANT: VENTER.

JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

JITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PAPELICATION NUMBER: 05/241,755

PRIOR PAPELICATION NUMBER: 60/241,755

PRIOR PAPELICATION NUMBER: 60/237,768

PRIOR PAPELICATION NUMBER: 60/231,498

PRIOR PAPELICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 17361

LENGTH: 767677
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                                                                        Sequence 17361, Application US/09949016 Patent No. 6812339
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; OTHER INFORMATION: n = A,T,C or G
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Oy 278 ProProThrThrLeuIleSerThrValPheThrargAlaAlaAlaAhrLeuGlnAlaMet 297	Oy 298 Ala	Oy 305 ThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320	Qy 321 ProPheThrGluIleSerAsnLeuThrLeuAsnThr332	Qy 333GlyAsnValTyrAsnProThrAlaLeuSerMetSerAsnValGluSer 348	Qy 349 SerThrMetAsnLysThrAlaSerTrpGluGlyArgGluAlaSerProGlySerSerSer 368	Oy 369 GlnGlySer-ValProGluAsnGlnTyrGlyLeuProPheGluLy8 383	RESULT 15 US-09-854-133-158/c ; Sequence 158, Application US/09854133 ; Patent No. 6759508	GENERAL INFORMATION: ; APPLICANT: Lodes, Michael J. ; APPLICANT: Mohamath, Raodoh ; APPLICANT: Henderson, Robert A. ; APPLICANT: Benson, Darin R.	; APPLICANT: Secrist, Heachiner ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER ; FILE REFREENCE: 210121.475C10 ; CURRENT APPLICATION NUMBER: US/09/854,133 ; CURRENT FILING DATE: 2001-05-11 ; NUMBER OF SEQ ID NOS: 735 ; SOFTWARE: FASISEQ for Windows Version 3.0 ; SRD 1D NO 158	; LENGTH: 214 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-854-133-158	Alignment Scores:  Pred. No.:  Score:  Score:  Autches:  Farent Similarity:  Best Local Similarity:  Query Match:  Autches:  Conservative:  Mismatches:  G.58  Gaps:  A Gaps:	US-10-735-014-83 (1-431) x US-09-854-133-158 (1-2114)	Oy 204 SerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuProGluAsnVal 223	Qy 224 SerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAlaThrPro 242	Oy 243 LysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSerGlnPro 262

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US-09-990-438-514
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Patent No. US20020058309A1
GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                             DB
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APPLICANT: Botstein, David
                             Length
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                                                                     Gurney, Austin
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Roy, Margaret
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kljavin, Ivar
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      Query
Match 1
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    Result
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-MODEL=frame+-pl2.model -DEV=xlp
-MODEL=frame+-pl2.model -DEV=xlp
-C-GPIZ 1/USPTO spool p/US10735014/runat_26042005_113103_7512/app_query.fasta_1.583
-D=-CGPIZ 1/USPTO spool p/US10735014/runat_26042005_113103_7512/app_query.fasta_1.583
-D=-Dublished Applications NA -QFPWT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCIL-0 -LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR GOCRE-pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFWT=pct -NORM=ext -HEAPSTEE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10735014 @CCN 1 1 723 @runat 26042005 113103_7512
-NCPU=5 -ICPU=3 -NO MMAP -LARGEQUERY NEG GCORES=0 -WAIT -DSPBLOGCR=100
-LONGLOG -DEV TIREOUT=120 -WARN TIMBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPEOR=6 -FGAPEXT=7 -YGAPOP=10 - YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                    (without alignments)
4063.079 Million cell updates/sec
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                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCTNEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                       nucleic search, using frame_plus_p2n model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Database

Total number of

Perfect score:

Sequence:

OM protein -

Run on:

Scoring table:

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Mucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PITC63
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                      AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle
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Patent No. US20020072067A1
GENERAL INFORMATION:
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Gurney, Austin L.
Kljavin,Ivar J.
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Botstein, David
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 82
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| Patent No. US20020072092A1 |
| Patent No. US20020072092A1 |
| APPLICANT: Ashkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Bosteein, David APPLICANT: Bestor, Mary Loan APPLICANT: Eaton, Dan L. APPLICANT: Ferrara, Napoleone APPLICANT: Fong, Sherman APPLICANT: Gerber, Hanspeter APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Goddwski, Paul J. APPLICANT: Goddwski, Paul J.
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         R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

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R APPLICATION NUMBER: 60/091544

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APPLICATION NUMBER: 60/088861
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
      Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                            SerLysProThrAsplleSerTrpArgAspThrLeuSerGlnLysPheGlySerAsp
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Patent No. US2002072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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R FILING DATE: 1998-06-24

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	APPLICANT: Pan, James APPLICANT: Paon, Nicholas F. APPLICANT: Roy, Margaret Ann APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K. APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I.	OF INVENTION: Secreted and OF INVENTION: Secreted and OF INVENTION: Acids Encodistrance: P2730PIC65 IT APPLICATION NUMBER: US/09 IT FILING DATE: 2001-11-19 APPLICATION NUMBER: 60/0497 FILING DATE: 1997-06-16	REIGN FILING DATE: 1997-10-17  REIGN FILING DATE: 1997-11-12  REIGN FILING DATE: 1997-11-12  REIGN RAPLICATION NUMBER: 60/065311  REIGN RAPLICATION NUMBER: 60/065710  REIGN BAPLICATION NUMBER: 60/06770  REIGN PAPLICATION NUMBER: 60/0779  REIGN RAPLICATION NUMBER: 60/075945  REIGN RAPLICATION NUMBER: 60/075945  REIGN RAPLICATION NUMBER: 60/075945  REIGN RAPLICATION NUMBER: 60/075945  REIGN RAPLICATION NUMBER: 60/076910		APPLICATION NUMBER: 60/ PILING DATE: 1998-06-02 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/ PILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/	PRIOR APPLICATION NUMBER: 60/088028 PRIOR PILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088029 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088030 PRIOR FILING DATE: 1998-06-04 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/088033 PRIOR PILING DATE: 1998-06-04 PRIOR PILING DATE: 1998-06-04 PRIOR PILING DATE: 1998-06-04 PRIOR PILING DATE: 1998-06-04

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	121 ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer 140	SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp	201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluleAlaHisLeuLeuPro 220	41 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 26	281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300	321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340	361 GlualaSerProGlySerSerSerGlnGlySerValProGluAsnGlnTyrGlyLeuPro 380  1306 GAGGCCAGTCCAGGCAGTTCCTCCAGGCAGTGTTCCAGAAATCAGTACGCCTTTCA 1365  381 PheGluLySTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuValIleGly 400  1366 TTGAAAAATGGCTTCTTATCGGGTCCTTTGGTGTCTGTTCCTGTGTGATAGGC 1425  401 LeuValLeuLeuGlyArglleLeuSerGluSerLeuArgArgLySArgTytSerArgLeu 420  1426 CTGTCCTCTGGGTAAAATCGGAAATCCTTCGGAAAAGTTAGTGTGATAGTG 1485  421 ABPTytLeuIleAsnGlyIleTytValAspIle 431
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PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: PAT/US99/1252
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PILING DATE: No. US20020102647Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PECTUARY 21, 2000
PRIOR APPLICATION NUMBER: PCT/US09/03565
PRIOR APPLICATION NUMBER: PCT/US09/0365
PRIOR APPLICATION NUMBER: PCT/US09/04414
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR APPLICATION NUMBER: PCT/US00/06441
PRIOR APPLICATION NUMBER: PCT/US00/06441
PRIOR PILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: May 28, 2000
PRIOR PILING DATE: DATE: PCT/US00/20710
PRIOR PILING DATE: PEDTUARY 28, 2001
PRIOR PILING DATE: PEDTUARY 28, 2001
PRIOR PILING DATE: PEDTUARY 28, 2001
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Conservative:
Mismatches:
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; ORGANISM: Homo Sapien
US-09-944-449-82
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Best Local Similarity:
Query Match:
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PELICANT: Wass, Daliel

TITLE OF INVENTION: SECRETE DA DU TRANSHERRANE POLYPEPTIDES AND NUCLEIC

FILE REPERENCE: P2548PIL MISS.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPERENCE: P2548PIL MISS.

CURRENT FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

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PRIOR FILING DATE: December 1, 1997

PRIOR FILING DATE: December 1, 1997

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PRIOR FILING DATE: PED-LANTY 9, 1998

PRIOR FILING DATE: PED-LANTY 9, 1998

PRIOR FILING DATE: December 1, 1997

PRIOR FILING DATE: PED-LANTY 9, 1998

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PRIOR PILING DATE: PED-LANTY 9, 
                1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
                                                                                                            1-09-944-449-82
Sequence 82, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
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Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
                                                                                                                                                                                                                                                                                                                                                Ferrara,Napoleone
Filvaroff,Ellen
                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Goddard, Audrey
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Tumas, Daniel
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: P2730P1C70 CURRENT APPLICATION VMBER: US/09/989,731 CURRENT FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/062260
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PAPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-10-2-6
PRIOR PILING DATE: 1998-02-25
PRIOR PAPLICATION NUMBER: 60/078910
PRIOR PILING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084500
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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APPLICATION UNMBER: 60/088202
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088326
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Grimaldi, J.Christopher
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Watanabe, Colin K.
Williams, P. Mickey
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Stewart, Timothy,
Tumas, Daniel
           Ferrara,Napoleone
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                                                                Gerber, Hanspeter
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Napier, Mary A.
                                       Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1006 CAGCCACAGGCCACCACCACCACCACGTAAACCACTGTCACTTCTCAGCCTCCCACG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCTCATTTCTACAGTTTTTACACGGGTGCGGGTACACTCCCAAGCAATGGCTACAACA 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGTTTACAGAAATCTCCAACTTAACTTTGAACACAGGAATGTGTATAACCCCTACTGCA 1245
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                                                                                    LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
                                                                                                                      CICITACATGGCCAATITICACAAGCAGTCACTCCCCTAGCCCATCATCACACAGATTAT 705
                                                                                                                                                                                                  SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAsnValSerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnProGlnLeuAlaThrAlaProProValThrThrValThrSerGlnProProThr 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
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LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro
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Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Bakenzi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, luc
APPLICANT: Baten, David
APPLICANT: Baton, David
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PRIOR APPLICATION NUMBER: 60/09045
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
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PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090676
PRIOR PILING DATE: 1998-06-25
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Alignment Scores:
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Query March: 100.00\$
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9 Gaps: 0

US-10-735-014-83 (1-431) x US-09-989-731-514 (1-2284)

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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US98/25108
                    Sequence 82, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
                                                                                               APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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                               466 TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCCAACTGCTACCTATTTTTCTGT 525
                                                                                               ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArg1le11e 120
                                                                                                                            CCCAACGAGGAAGCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585
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LeuMet IlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P5248PL1
CURRENT PAPLICATION NUMBER: US/09/944,457
CURRENT PAPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-09-26
PRIOR PLILING DATE: 2001-09-26
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PRIOR PLILING DATE: December 11, 1997
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PRIOR PLILING DATE: PECADER 18, 1998
PRIOR PLILING DATE: PECADER 29, 1998
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                LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr
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Sequence 514, Application US/0989732

Patent No. US20020123463A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Bester, Kevin P.

APPLICANT: Bester, Lavin C.

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Foreara, Napoleone

APPLICANT: Gerber, Hanspeter
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PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR PLILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR APPLICATION NUMBER: PCT/US99/28419
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: No. US20020110859Alember 30, 1999
PRIOR PILING DATE: No. US20020110859Alember 30, 1999
PRIOR PILING DATE: No. US20020110859Alember 30, 1999
PRIOR PILING DATE: No. US20020110859Alember 30, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR PILING DATE: Pebruary 21, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/08419
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR PILING DATE: March 30, 2000
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PRIOR APPLICATION NUMBER: PCT/US00/2678
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PRIOR APPLICATION NUMBER: PCT/US00/06520
PRIOR PILING DATE: PEDRUARY 28, 2001
PRIOR FILING DATE: PEDRUARY 28, 2001
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Best Local Similarity:
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R APPLICATION NUMBER: 60/088976
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R FILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090472
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LICATION NUMBER: 60/089598
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091CS:
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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NG DATE: 1997-11-24
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APPLICATION NUMBER: 60/088021
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                                Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                        Napier, Mary A.
Pan, James
Paoni, Nicholas F.
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                                                                       javin, Ivar J
                   Godowski, Paul
                                                                     APPLICANT:
APPLICANT:
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                  ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArg1leIle
                                                                                              HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu
                                                                                                                                                                                                                                                                                                                   LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro
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                                            526 cccaaccaggaagccrgrccarrgaaaccagcaaaaggacrrargagrracaggaraarr
                                                                           ThrAspPheProSerLeuThrArgAsnLeuProSerGlnGluLeuProGlnGluAspSer
                                                                                                                                     LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr
                                                                                                                                                                                                SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp
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US-09-991-073-514
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; Patent No. US20020127576A1
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          R APPLICATION NUMBER: 60/090535
R FILING DATE: 1998-06-24
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R APPLICATION NUMBER: 60/090542
R APPLICATION NUMBER: 60/090557
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R APPLICATION NUMBER: 60/090676
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R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/091360

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091478

R FILING DATE: 1998-07-01

R APPLICATION NUMBER: 60/091549

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APPLICATION NUMBER: 60/092182
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PILING DATE: 1998-06-10
APPLICATION NUMBER: 60/089826
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090355
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088861
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088734
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PICLS
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PRIOR APPLICATION NUMBER: 05/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Gerritsen, Mary E
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                                        Baker, Kevin P.
Botstein, David
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                                                                                                                                                                                               Fong, Sherman
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PRIOR APPLICATION NUMBER: 60/090431 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PELLOATION NUMBER: 60/090435 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-25	APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0	## PRIOR PEDIGATION NUMBER: 60/092182  ### Alignment Scores:   1.47e-21

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PRIOR PAPLICATION NUMBER: 00/060, 131
PRIOR PELLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR PELLING DATE: December 11, 1997
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                                    1486 GATTATTTGATCAATGGGATCTATGTGGACATC 1518
421 AspTyrLeuIleAsnGlyIleTyrValAspIle
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FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
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                                                                                                                                                                                    Sequence 82, Application US/09945587
Patent No. US20020127643A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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APPLICANT: Botstein, David
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Goddard, Audrey
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Tumas, Daniel
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LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys 100
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PRIOR FILING DATE: Warch 3, 1999
PRIOR PELING DATE: June 22, 1999
PRIOR PELING DATE: June 22, 1999
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PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US2002012/643Alember 30, 199
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PRIOR FILING DATE: No. US2002012/643Alember 30, 199
PRIOR FILING DATE: December 1, 1999
PRIOR PELING DATE: December 1, 1999
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PRIOR FILING DATE: PEDTUARY 11, 2000
PRIOR FILING DATE: PEDTUARY 11, 2000
PRIOR FILING DATE: PEDTUARY 22, 2000
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PRIOR PELING DATE: MARCH 30, 2000
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PRIOR PELING DATE: PEDTUARY 28, 2001
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LING DATE: December 16, 1998
PLICATION NUMBER: 09/218,517
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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CURRENT PELLING DATE: 2011-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
                                                                                    Ferrara, Napoleone
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Stewart, Timothy
Tumas, Daniel
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Napier, Mary A.
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                              Desnoyers, Luc
Eaton, Dan L.
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                                                                                                                                                        LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisThrAspTyr 160
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CCCAACGAGGAAGCCTGTCCATTGAAACCAGCAAAAGGACTTATGAGTTACAGGATAATT 585
                                                                                                                                                                                                                                                                        SerLysProThrAspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180
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                                                        ThraspPheProSerLeuThrargasnLeuProSerGlnGluLeuProGlnGluAspSer
                                                                                    586 ACAGATTTTCCATCTTTGACCAGAAATTTGCCAAGGCAAGGAGTTACCCCCAGGAAGATTCT
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Sequence 514, Application US/09990442 Patent No. US20020112252A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.

Baker, Kevin P.

APPLICANT:

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202 212 217 217 734 738 742 742 810 824 826	858 861 876 105 105 512 512 538 538	599 600 653 801 907 947 948	90246 90252 90254 90349 90355 90429
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Percent Similarity:	100.00\$	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00\$	Indels:	0
DB:	6	Gaps:	0
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1 Metphephe 226 ATGTTCTTC 21 LeuArgLet 	1 MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuValllelleCysPheLeuThr 20	26 ATGTTCTTCGGGGGAGAAGGTTTGACTTACACTTTGGTAATATTTGCTTCCTGACA 28> 21 LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp 40	CTAAGGCTGTCTGCTAGTCAGAATTGCCTCAAAAGAGTCTAGAAGATGTTGTCATTGAC 345	41 IleGInSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln 60	346 ATCCAGTCATCTTTTTTTTTTTAAGGAATCAGAGGCAATGAGGCCCGTATATACTTCAACTCAA 405	61 GluAspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80
1 226 21 286 41 41 346	MetPhePheGlyGlyG	ATGTTCTTCGGGGGAG. LeuArgLeuSerAlaS	CTAAGGCTGTCTGCTA		ATCCAGTCATCTCTTT	GluAspCysIleAsnS
	7	226	286	41	346	61

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APPLICANT: Turas, bantel
APPLICANT: Turas, bantel
APPLICANT: Wetanabe, Colin K.
APPLICANT: Wetanabe, Colin K.
APPLICANT: Wickey
APPLICANT: Wickey
APPLICANT: Wood, Williams P. Wickey
APPLICANT: Abang, Zemin
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION WOMER: US/09/991.163
CURRENT APPLICATION NUMBER: 60/049707
PRIOR PILLING DATE: 1997-10-11
PRIOR APPLICATION NUMBER: 60/06230
PRIOR PILLING DATE: 1997-10-12
PRIOR APPLICATION NUMBER: 60/063311
PRIOR APPLICATION NUMBER: 60/08312
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                                            RESULT 13
US-09-991-163-514
US-09-991-163-514
Sequence 514, Application US/09991163
Fabrent No. US20020132533A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Stewart, Timothy A.
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Watanabe, Colin K.
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Gerber, Hanspeter
Gerritsen, Mary E
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Botstein, David
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PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: July 28, 1999
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: September 16, 1998
PRIOR FILING DATE: December 16, 1998
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PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR APPLICATION NUMBER: PCT/US99/28009
PRIOR FILING DATE: No. US200201376844ember 30, 1999
PRIOR FILING DATE: No. US200201376844ember 30, 1999
PRIOR FILING DATE: No. US200201376844ember 30, 1999
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDULARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08419
PRIOR APPLICATION NUMBER: PCT/US00/08419
PRIOR FILING DATE: FEDRUARY 22, 2000
PRIOR PRIOR FILING DATE: PEDULARY 21, 2000
PRIOR PRIOR FILING DATE: PEDULARY 21, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: PEDULARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: PEDULARY 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
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Application US/09944396
                              Perrara, Napoleone
Filvaroff, Ellen
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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               APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
                                                              Gurney, Austin
Hillan, Kenneth
Sequence 82, Application U
Patent No. US20020132981A1
GENERAL INFORMATION:
                                                                         Kljavin, Ivar
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226 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA 285
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PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: June 22, 1999
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR PELICATION NUMBER: PCT/US99/2813
PRIOR PELICATION NUMBER: PCT/US99/2813
PRIOR PELICATION NUMBER: PCT/US99/2813
PRIOR PILING DATE: No. US20020132981Alember 30, 1999
PRIOR FILING DATE: No. US20020132981Alember 30, 1999
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PELICATION NUMBER: PCT/US90/03565
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PILING DATE: PEDRUARY 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PELICATION NUMBER: PCT/US00/08439
PRIOR PELICATION NUMBER: PCT/US00/14042
PRIOR PELICATION NUMBER: PCT/US00/20710
PRIOR PELICATION NUMBER: PCT/US00/20710
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
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PRIOR PILING DATE: PROFICE ADDITION NUMBER: PCT/US00/20710
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; ORGANISM: Homo Sapien
US-09-944-396-82
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Ор	706 TCAAAGCCC	
δ	-	LysteuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200
Op	99	CACCTGGAGAAACTATTAAGATGGATGGAAGTGCCCAGCTCCTTGCTTATAAGGAA 825
ò	201 LysglyHig	SerGinSerSerGinPheSerSerAspGlnGluileAlaHisLeuLeuPro 220
Dp	826 AAAGGCCAT	AAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCCT 885
ò	221 GluAsnVal	SerAlaLeuProAlaThrValAlaValAlaSerProHisThrThrSerAla 240
QΩ	886 GAAAATGTC	GAAAATGTGAGTGCGCTCCCAGCTACGTGGCAGTTGCTTCCCACATACCACCTCGGCT 945
δ	241 ThrProLys	PProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260
qq	946 ACTCCAAAC	ACTCCAAAGCCCGCCACCTTCTACCCACCATGCTTCAGTGACACCTTCTGGGACTTCC 1005
ζŏ	261 GlnProGlr	ILEUA  2ThrThrA  aProProVa  ThrVa  ThrSerG  nProProThr 280
Db	1006 CAGCCACAG	
à	281 ThrLeuile	SerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
ДD	1066 ACCCTCATT	
ò	301 AlaValLet	ThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
qq	1126 GCAGTTCTC	
ογ	321 ProPheThr	GlulleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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λ̈́o	341 LeuSerMet	SerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360
Dþ	1246 CTTTCTATG	
δ	361 GluAlaSer	GluklaSerProGlySerSerSerGlnGlySerValProGluksnGlnTyrGlyLeuPro 380
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δλ	381 PheGluLys	TrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVallleGly 400
Dp	w	H
ò		LeuGlyArglleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
Db	1426 CTCGTCCTC	CTCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTG 1485
δλ		AspTyrLeulleAsnGlyIleTyrValAspIle 431
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CC0979641 BOVGen 07
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1 (bases 1 to 1296)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu.F., Murphy, B., Perriera, S., Wanong, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargili, Ne.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Birect Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Homo sapiens HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
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-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-G-cgnz_1/USFTO_spool_p/US10735014/runat_26042005_113101_7425/app_query.fasta_1.583
-G-cgnz_1/USFTO_spool_p/US10735014/runat_26042005_113101_7425/app_query.fasta_1.583
-DEST -CPRYT=fastap -SUFFTX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOALIGN=200 -THR_SCORE=pct -THR MAX=100 -THR MINO -ALIGN=15 -MODE=LOCAL
-UOTFRY=pcto -NORM=ext -HEAPSIZE=50 -MINIEN=0 -MAXIEN=200000000
-USER=US10735014 @CGN 1 1 5180 @runat_26042005 113101 7425 -NCPU=6 -ICPU=3
-NO_MMAP -LARREGOUERY -NEG SCORES=0 -WAIT -DSPBALOK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                    - nucleic search, using frame_plus_p2n model
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Matches:
Conservative:
Mismatches:
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1296 bp DNA linear GSS 12-DEC-2003
Pan troglodytes HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY401137
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                                                                                                                   321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
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                                                         301 AlaValLeuThrThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320
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GSS.

Ban troglodytes (chimpanzee)
Pan troglodytes
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Pan.

[1 (bases 1 to 1296)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wanghy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGTTCTGACTACCACCTTTCAGGCACCCTACGGACTCGAAAGGCAGCTTAGAAACCATA
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Qy         321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340           Db         961 CCGTTACAGAAATCTCCAACCTTAGACACAGGAATGTGTATAACCCTACTGCA 1020           Qy         341 LeuSerMetSerAsnValGluSerSerThrMetAsnLysThrAlaSerTrpGluGlyArg 360           Db         1021 CTTTCTATGTAGTGCAGACTCTCCACTACGAATAAACTGCTTCCGGAAATAAGG 1080           Qy         361 GluAlaSerProGlySerSerSerSerGluGlySerValProGluAsnGradG 1080           Qy         361 GluAlaSerProGlySerSerSerSerGluGlySerValProGluAsnGluTyrGlyLeuPro 380           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 381 PheGluLysTrpLeuLeuIleGlySerLeuLeuPheGlyValLeuPheLeuVall1eGly 400		RESULT 3 CR621081 LOCUS CR621081 DEFINITION full-length cDNA clone CSODIO54YH07 of Placenta Cot 25-normalized	ACCESSION CR621081 VERSION CR621081.1 GI:50501888 KEYWORDS HTC; CNSLT_cDNA.	Σ	E 1 (bases 1 to 1965) S Li,W.B., Gruber,C., Jessee,J. Full-length cDNA libraries ar L Unpublished		AUTHORS Genoscope.  TITLE Direct Submission JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	ပည	was normalized. Library was constructed by Lire Technologies, a division to Invitrogen. FEATURES Location/Oualifiers source 11965		/tissue_type="lacenta_cot_25-normalized" /plasmid="pCMVSPORT_6" ORIGIN	Alignment Scores: 3.05e-156 Length: 1965 Pred. No.: 1831.00 Matches: 357 Percent Similarity: 100.00% Conservative: 0	: 100.00% Mismatches: 82.81% Indels: 3 Gaps: 31) x CR621081 (1-1965)
9.96e-189 Length: 1296 2183.00 Marches: 426 2183.00 Marches: 426 30.84\$ Conservative: 0 9.73\$ Indels: 0 9 Gaps: 0 -83 (1-431) x AY401137 (1-1296) MetPhepheGlyGlyGsrLeuThrTyrThrLeuValllelleCysPheLeuThr	21 21 61	Qy         41 IleGlnSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln 60           Db         121 ArCCAGTCATCTTTTTTAAGGGAATGAGCCGTATAATCTTCAACTTCAA 180           Qy         61 GluAspCysILeAsSerCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn 80           Cb         181	Qy       81 LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys       100         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120	Qy       121 ThråspPheProSerLeuThrårgåsnLeuProSerGinGluLeuProGlinGluÅspSer 140         Db       361 ACAGATTTCCATCTTTGACCAGAAATTTGCCAAGAGTTACCCCAGGAAGATTCT 420	Oy     141 LeuLeuHisGlyGlnPheSerGlnAlaValThrProLeuAlaHisHisHisHhrAspTyr 160       Db     421 CTCTTACATGGCCAATTTTCACAAGCAGTCACCCCTAGCCCATCATCACACAGATTAT 480	Oy 161 SerLysBroThraspIleSerTrpArgAspThrLeuSerGlnLysPheGlySerSerAsp 180	Oy 181 HisLeuGluLysLeuPheLysMetAspGluAlaSerAlaGlnLeuLeuAlaTyrLysGlu 200	Qy       201 LysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGluIleAlaHisLeuLeuPro       220         Db       601 AAAGGCCATTCTCAGAGTTCACAGTTTTCCTCTGATCAAGAAATAGCTCATCTGCTGCT       660	Qy       221 GluasnvalseralaLeubroAlaThrValAlaValAlaSerProHisThrThrSerAla 240         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy     241 ThrProLysProAlaThrLeuLeuProThrAsnAlaSerValThrProSerGlyThrSer 260       Db     721 ACTCCAAAGCCCACCACCACCACCACCACCATGCTTCAGGACTTCC 780	Qy         261 GlnProGlnLeuAlaThrThrAlaProProValThrThrValThrSerGlnProProThr 280	ThrLeulleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 	Oy 301 AlavalLeuThrThrThePheGlnAlaProThrAspSerLysGlySerLeuGluThrIle 320 

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18 I (bases I to 833)

18 NIH-MGC http://mgc.nci.nih.gov/.

18 National Institutes of Health, Mammalian Gene Collection (MGC)

18 National Institutes of Health, Mammalian Gene Collection (MGC)

19 Contact: Robert Strausberg, Ph.D.

19 Email: cgapbs-r@mail.nih.gov/

19 Tissue Procurement: ATCC/DCTD/DTP

19 CDNA Library Preparation: Life Technologies, Inc.

19 CDNA Library Preparation: Life Technologies, Inc.

10 CDNA Library Preparation: Life Technologies, Inc.

10 CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

10 A Sequencing by: Agencourt Bioscience Corporation

10 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

11 High quality sequence stop: 735.

12 Location/Qualifiers
AGENCOURT 7896936 NIH_MGC_72 homo sapiens cDNA clone IMAGE:6159709
5', mRNA Sequence.
BQ424639
EST.
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Matches:
Conservative:
Mismatches:
Indels:
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1376.00
99.28%
98.55%
62.23%
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Homo sapiens
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Best Local Similarity:
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LOCUS
DEFINITION
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SOURCE
ORGANISM
                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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Drimer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  Alignment Scores:  Alignment Scores:  Pred. No.:  Percent Similarity	Oy 125 SerleuThrarghanLeuProSerGlnGluLeuProGlnGluAspSerleuLeuHisGly 144		225 AlaLeuDroAlaThrValAlaValAlaSerProHisThrThrSerAlaThrProLysPro 216 GCGCTCCCGGCTACGGTGGCAGTTGCTTCTCCACATACCACCTCGGCTACTCCAAGCCC 217 AlaThrThrAlaProProValThrThrValThrProSerGlyThrSerGlnProGlnLeu 218 GCGCTCCCACCACCACCTCGCTTCACTCTCTCGGACTTCCCAGCTGCTGCTCCCACCTCGGCTTCCACCTCCGGCTACCTCCACCTCGGACTTCCCAGCTCCCACCTCGCACTTCTCCAGCTCCCACCACCTCCACCTCTCACCTTCTCTGGACTTCCCAGCTCCCACCACCTCCACCTCTTACACTTCTCAGCTCCCACCACCTCTTTTTTCTCTCTC
	Qy         253 SerValThrProSerGlyThrSerGlnProGlnLeuAlaThrThrAlaProProValThr 272           Db         557 TCAGTGACACTTCTGGGACTTCCCAGCTGGCCACCACCTCAGCTCCACCTGTAACC 616           Qy         273 ThrValThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAla 292           Db         617 ACTGTCACTTCTCAGCCTCCATTCTACAGGGCTGCGGT 676           Qy         293 ThrLeuIll	Qy         313 SerLysGlySerLeuGluThrIleProPheThrGluIleSerAsnLeuThrLeuAsnThr 332           Db         737 TCGAAAGGCTTAGAAACCATTACAGAAATCTCCCACTTAACTTTGAACAC 796           Qy         333 -GlyAsnValTyrAsn-ProThrAlaLeuSerMetSerAsnVal 346           Db         797 GGGGAATGTGTATACCCCTTACTGCACTTTCTATGTCAAATGTG 840	a o Tit dat Dar

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966 YWATGCMAARCCSGCAMCCTTYTACCCM---CAATGCTTAGTGAMACCTYYTGGACTYCM 1022
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Mus musculus HCM0790 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1245)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
   TTGATGATCTTCGACACTCGAAAAACAGCTAGACAACCCAACTGCTACCTATTTTTCTGT
                                                            ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle
                                                                                                                cccaacgaggaagccrgrrcarrgaaaccagcaaaaggacrrargagrracaggaraarr
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                                                                                                             AL525434 ALORO Sapiens NEUROBLASTOWA COT 25-NORMALIZED Homo sapiens CDNA clone CSODCOllYGO7 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens NEUROBLASTOMA_COT_25-NORMALIZED"
/note="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

( Dases 1 to 1050)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:31063298.
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/db_xref="taxon:9606"
/clone="CS0DC011YG07"
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93.13%
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AK033526

Mus musculus adult male colon cDNA, RIKEN full-length enriched ibrary, clone:9030601P12 product:weakly similar to NT2RM1001115 PROTEIN (Homo sapiens), full insert sequence.

AK033526

AK033526.1 GI:26329204

HTC; CAP trapper.

Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
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     -CCCGTGGTTACACATCAG
                                   AlaValLeuThrThrPheGlnAlaProThrAspSerLysGlySerLeuGluThrIle
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High-efficiency full-length CDNA.
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia;
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NKTASWEDRRVSVGGASLNKGPKSQHGLSFEKWLLIGTLLGCVLFLVIGLVLLGRMLV
BALRRKRYSRLDYLINGIYVDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trissue type="colon"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein id="BAC28341.1"
/db_xref="G1:26329205"
/translation="MLFRGTSLAYSLLVISFLTPRSSAGQNCLTKSLEDVVIDIQSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGIRGNEPIHLATQEDCIGACCSTKDIAGDKACNLMIFPTRKTDRQPNCYLFFCPSE
DACPLKPAKGLVTYRLIRDFPLTSANSSLQQLTQGEFLLLDHSSPGATPGFRTPAGYP
                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Stanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2235)
                                                                    Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; putative weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR|QONW60, evidence: FASTY, 58.3%ID, 96.7%length,
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                    Exploration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site for further details.
URL:http://ganome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                    Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/etrain="C57BL/6J"
/db_xref="RANTOM DB:9030601P12"
/db_xref="taxon:10090"
/clone="9030601P12"
                                                                    The FANTOM Consortium and the RIKEN
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Pred. No.:
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        TITLE
JOURNAL
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AUTHORS
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JOURNAL
                                                                 AUTHORS
                                                                                                                                                JOURNAL
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Length:

3.46e-95

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JOURNAL Nature 420, 563-573 (2002)  Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakhors Adachi,J., Aizawa,K., Akahira,S., Pikuda,S., Fukudishi,Y., Fukudishi,Y., Fukudishi,Y., Fukudishi,Y., Haracka,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Haracka,T., Hori,P., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Tumission of Direct Submission of Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Yokohama, Institute, I722 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@ggc.riken.jp,	URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)  COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.  CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAAGAACACTCTTTTTTTTTTTTTTTTTV 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.2. Second strand cDNA was prepared with the primer adapter of sequence [5'	GAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCC	CDS 2621506  Anote="unnamed protein product; putative weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR   O9NW60. evidence: FASTY, S8.3%ID, 96.7%length, match=1104] (SPTR   O9NW60. evidence: FASTY, S8.3%ID, 96.7%length, match=1104]    Amoth=1104]   Amoth=1104]   Amoth=1104   Am
ADG ADG ADG ADG ADG ADG ADG ADG ADG ADG	SE CO	PEAT	ORIGIN Alignm Pred. Score: Percen
	Db 1492 GACTACTTGATCAACGGGATCTATGTTGACATC 1524  RESULT 9  AK018635  LOCUS  AK018635  AK018635  LOCUS  AK018635  AK018635  AK018635  AK018635  AK018635  AK018635  ACCESSION  AK018635  ACCESSION  AK018635  ACCESSION  AK018635  ACCESSION  AK018635  AK018635  ACCESSION  AK018635  AK018635  AK018635  AK018635  AK018635  AK018635  AK018635  AK018635  AK018635  AKO18635	utheria; Rodentia; Sciurognathi; Murida, and Hayashizaki, Y. ency full-length cDNA cloning iol. 303, 19-44 (1999)  , Shibata, Y., Hayatsu, N., Sugahara, Y., mno, H., Okazaki, Y., Muramatsu, M. and Ha con and subtraction of cap-trapper-selection and subtraction of cap-trapper-selection (10), 1617-1630 (2000)	AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashino,H., Itoh,M., Yamanoto,R., Jaki,M., Nishino,T., Harada,A., Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yamanoto,R., Indikawa,T., Ozawa,Y., Izawa,M., Ohara,E., Warahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tranaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer of pipeline with 384 multicapillary sequencer of 50530913  MEDLINE 20530913  THILE 20530913  THYROR Consortium.  TITLE Punctional annotation of a full-length mouse cDNA collection JOURNAL Nature 409, 685-690 (2001)  REFERENCE The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

us-10-735-014-83.rst

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SKGIRGNEPIHLATGEDCIGACCSTKDIAGDKACNLMIFDTRKTDRQPNCYLFFCPSE
DACPLKRPAKGLTYRLIRDFPLTSANSLOQITGREFLLLDHSSPGATPGFRFPAGYP
KPTGLSWSDRSSLKSTAPLHIRKHIKADETSWQLPEEKSHSQSLQLPSELKWAHLLPK
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                                                                                                                                                                                                                             Direct Submission in Appaintent; 1.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
             Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nashi, X., Myazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Tokahashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                      Riken
                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; putative
weakly similar to NT2RM1001115 PROTEIN [Homo sapiens]
(SPTR|Q9NW60, evidence: FASTY, 58.3%ID, 96.7%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2265
258
37
119
17
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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2265
/note="putative"
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1164.50
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Best Local Similarity:
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DB:
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REFERENCE
AUTHORS
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1127 GCAGCTTTGACTAACACCTTTCAGGCACATACAGACTCCAAAGGCATCTTAGAAACAATG 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 ThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeuGlnAlaMetAlaThrThr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 ProPheThrGluIleSerAsnLeuThrLeuAsnThrGlyAsnValTyrAsnProThrAla 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 GluhlaSerProGlySerSerSerGlnGlySerValProGluhsnGlnTyrGlyLeuPro 380
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                                                                                                                                     CCAAGGTCGTCGCTGGTCAGAACTGCCTCACCAAGAGTCTAGAAGACGTTGTCATTGAC
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                                                                                                                                                                                                                                                                              Arccaarcercecrircaaaaeecarrceaeecaareaeccearacacrreecaacrcae
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                                                                                              LeuArgLeuSerAlaSerGlnAsnCysLeuLysLysSerLeuGluAspValValIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuMetIlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGATGATCTTTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACCTGTTTTTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArglleIle
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Sogabe, Y.,

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                                                                                       Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Exploration Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Wihittp://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cecum"
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                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.jp/) for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; putative weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR|Q9NW60, evidence: FASTY, 58.3%ID, 96.7%length,
     Sano, H., Sasaki, D.,
                       Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                            TITLE
JOURNAL
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1289 AGGGTCAGTGTAGGCAGCGCATCGCTGAACAAGGGTCCAAAAAGCCAGCATGGCCTTTCA 1348
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                                                                                                                                                                                 1409 CTCGTCCTCTTGGGTAGGATGCTGGTTGAAGCCCTCCGTAGGAAACGGTATTCAAGACTT 1468
                                                                                                                                                                                                                                                                                                                                                                                                            HTC 03-APR-2004
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                                                                                                                                                    LeuValLeuLeuGlyArgIleLeuSerGluSerLeuArgArgLysArgTyrSerArgLeu 420
                                                    PheGluLysTrpLeuLeulleGlySerLeuLeuPheGlyValLeuPheLeuVallleGly 400
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Inalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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      ATCCAATCGTCGCTTTCAAAAGGCATTCGAGGCAATGAGCCCATACACTTGGCAACTCAG
                                               GludspCysIleAsnSerCysCysSerThrLysAsnIleSerGlyAspLysAlaCysAsn
                                                                          LeuMet IlePheAspThrArgLysThrAlaArgGlnProAsnCysTyrLeuPhePheCys
                                                                                                                                                            TTGATGATTGACACCCGGAAGACAGACAGACAGCCCAACTGCTACTTTTTCTGT
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BGSTSRTPVATHQAALTNTRQHTDSKGILETMPFQGGSTLTSDPRHGKSSTSBSSIT
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Takahashi,F., Takaku-Akahira,S.,
Toya,T., Yasunishi,A.,
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/note="unnamed protein product; putative
weakly similar to NT2RM1001115 PROTEIN [Homo sapiens
(SPTR|Q9NW60, evidence: FASTY, 58.3%ID, 96.7%length,
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|clone_lib="RIKEN full-length enriched mouse
|dev_stage="adult"
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Conservative:
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Indels:
Sogabe, Y., Tagami, M., Tagawa, A.,
Atakeda, Y., Tanaka, T., Tomaru, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
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CFS95929 753 bp mRNA linear EST 26-SEP-2003
AGENCOURT_15668985 NCI CGAP_St3 Homo sapiens cDNA clone
IMAGE:30703562 5', mRNA sequence.
                                            101 ProAsnGluGluAlaCysProLeuLysProAlaLysGlyLeuMetSerTyrArgIleIle 120
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloA07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Arnold Schwartz, MD, PhD
CDNA Library Preparation: CLONTECH Laboratories, Inc.
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CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:
http://image.llnl.gov
Plate: NDCM251 row: d column: 03
High quality sequence stop: 540.
Location/Qualifiers
                                                                                                                                                                                                                                                                  181 GAAGACTGCATTAATTCTTGCTGTTCAACAAAAAACATATCAGGGGACAAAGGCATGTAAC
                                                                                                                                        41 IleGlnSerSerLeuSerLysGlylleArgGlyAsnGluProValTyrThrSerThrGln
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1 ATGTTCTTCGGGGGAGAAGGGAGCTTGACTTACACTTTGGTAATAATTTGCTTCCTGACA
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1 (bases 1 to 753)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                 EST 20-AUG-2004
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 623)

Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Vidal M
Marc Vidal Laboratory
Mana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 612 5180
Fax: 617 632 5739
Fax: 617 632 5739
GR Squence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetPhePheGlyGlyGluGlySerLeuThrTyrThrLeuVallleIleCysPheLeuThr 20
                                                                                                                                                            CV024215
1439 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC032998, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tisue type="mixed" /clone Tib="Full Length cDNA from the Mammalian Gene Collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 11036 row: 12 column: E
Seq primer: ACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAAC
High quality sequence start: 94
High quality sequence stop: 622
POLYANO.
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Mismatches:
Indels:
                   Std Error: 122.00
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Matches:
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SOWARD: ATGTTCTTCGGGGGGAAAGGGAG
BACKWARD: TAGATGTCCAGATAGACCCATI
INSERT LENGTH: 623 Std Error: 12
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/db_xref="taxon:9606"
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98.55%
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Homo sapiens
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Query Match:
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FEATURES

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The FANTOM Consortium and the RIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas

Nature 420, 563-573 (2002)

E 6 (bases 1 to 2227)

SA Achi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Purno, M., Hansagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Managaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiramoto, K., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Tagami, M., Tagawa, A., Takahashi, F., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Direct Submission and Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                          AK002644

2227 bp mRNA linear HTC 03-APR-2004
MNB musculus adult male kidney cDNA, RIKEN full-length enriched
library, clone:06100179409 product:weakly similar to NT2RM1001115
PROTEIN [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Aliyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suhi, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazali, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General General
  605 AATCAGTACCGCCTTCCATTTGAAAAATGGCTTCTTATCGGGTCCCTGCCTTTTGGGTG 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                                                                                                       AX002644.1 GI:12832780
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
                                                      394 alLeuPhe 396
                                                                                                      665 récrerre 672
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VERSION
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                                                                                                                                                            RESULT 15
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             /organism="Homo sapiens"
//organism="Homo sapiens"
//dol_type="mRNA"
//db_xref="Laxon:9606"
//dlone="TMAGE:30703562"
/tissue_type="Stomach, adenocarcinoma"
/tab host="bH10B (TT phage-resistant)"
/clone_lib="NCI_CAAP_E13"
/note="Vector: pDNR-LIB; Site_1: Sfi! (ggccattatggcc);
Site_2: Sfi! (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGCCATARIGGCC-3' and 3' adaptors sequence:
5'-CACGCCATARIGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCAGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average innert size 1.30
kb (range 0.60-3.5 kb): 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ThrSerGlnProProThrThrLeuIleSerThrValPheThrArgAlaAlaAlaThrLeu 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 ACTICTCAGGCCTCCCACGACCTCTATTTTACAGGCTGCGGCTACACTC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnAlaMetAlaThrThrAlaValLeuThrThrThrPheGlnAlaProThrAspSerLys 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 CAAGCAATGGCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGAACTCGAAA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 GGCAGCTTAGAAACCATACCGTTTACAGAAATCTCCCAACTTAACTTTGAACACAGGGAAT 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLeuAlaTyrLysGluLysGlyHisSerGlnSerSerGlnPheSerSerAspGlnGlu 214
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                                                                                   crcrrracrracarracricaccagascacciccragarracgracccasacarrac 756
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                                                                                                          Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .2227
/note="weakly similar to NT2RM1001115 PROTEIN [Homo sapiens] (SPTR|Q9NW60, evidence: FASTY, 58.3%ID,
96.7%length, match=1104)"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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